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(21) International Application Number: PCT/US98/24029 (22) International Filing Date: 10 November 1998 (10.11.1998) (60) Parent Application or Grant UNIVERSITY OF ROCHESTER [/]; (). ZAUDERER, Maurice [/]; (). STEFFE, Eric, K. ; ().		Published
(54) Title: T CELLS SPECIFIC FOR TARGET ANTIGENS AND METHODS AND VACCINES BASED THEREON (54) Titre: LYMPHOCYTES T SPECIFIQUES D'ANTIGENES CIBLE, VACCINS PREPARES A PARTIR DESDITS LYMPHOCYTES, ET METHODES ASSOCIEES		
(57) Abstract <p>The present invention relates to novel methods for the identification of antigens recognized by cytotoxic T cells (CTLs) and specific for human tumors, cancers, and infected cells, and the use of such antigens in immunogenic compositions or vaccines to induce regression of tumors, cancers, or infections in mammals, including humans. The invention encompasses methods for induction and isolation of cytotoxic T cells specific for human tumors, cancers and infected cells, and for improved selection of genes that encode the target antigens recognized by these specific T cells. The invention also relates to differential display methods that improve resolution of, and that reduce the frequency of false positives of DNA fragments that are differentially expressed in tumorous, cancerous, or infected tissues versus normal tissues. The invention further relates to the engineering of recombinant viruses as expression vectors for tumor, cancer, or infected cell-specific antigens.</p> (57) Abrégé <p>La présente invention concerne de nouvelles méthodes d'identification d'antigènes, reconnus par les lymphocytes T cytotoxiques (CTL), et spécifiques des tumeurs, cancers et autres cellules infectées chez l'homme, ainsi que l'utilisation de ces antigènes dans des compositions ou vaccins immunogènes pour induire une régression des tumeurs, cancers, ou infections chez les mammifères, notamment chez l'homme. L'invention concerne donc des méthodes permettant d'induire et d'isoler des lymphocytes T cytotoxiques spécifiques des tumeurs, cancers et autres cellules infectées chez l'homme, et de sélectionner de façon plus précise les gènes codant pour les antigènes cible reconnus par ces lymphocytes T spécifiques. L'invention concerne également des méthodes d'affichage différentiel améliorant la résolution des fragments d'ADN et réduisant la fréquence des faux positifs des fragments d'ADN exprimés de façon différentielle dans des tissus tumoraux, cancéreux ou infectés et dans les tissus normaux. L'invention concerne enfin la mise au point par génie génétique de virus de recombinaison faisant office de vecteurs d'expression pour les antigènes spécifiques des tumeurs, cancers et autres cellules infectées.</p>		

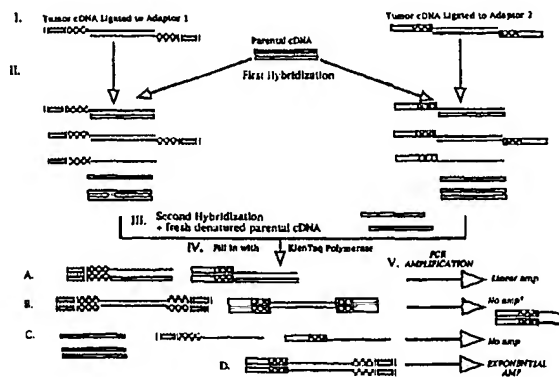
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(21) International Application Number: PC1/US98/24029 (22) International Filing Date: 10 November 1998 (10.11.98) (71) Applicant: UNIVERSITY OF ROCHESTER [US/US]; Office of Technology Transfer, 518 Hylan Building, Rochester, NY 14627 (US). (72) Inventor: ZAUDERER, Maurice; 44 Woodland Road, Pittsford, NY 14534 (US). (74) Agent: STEFFE, Eric, K.; Sterne, Kessler, Goldstein & Fox P.L.L.C., Suite 600, 1100 New York Avenue, Washington, DC 20005-3934 (US).	(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i>	

(54) Title: T CELLS SPECIFIC FOR TARGET ANTIGENS AND METHODS AND VACCINES BASED THEREON



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The present invention relates to novel methods for the identification of antigens recognized by cytotoxic T cells (CTLs) and specific for human tumors, cancers, and infected cells, and the use of such antigens in immunogenic compositions or vaccines to induce regression of tumors, cancers, or infections in mammals, including humans. The invention encompasses methods for induction and isolation of cytotoxic T cells specific for human tumors, cancers and infected cells, and for improved selection of genes that encode the target antigens recognized by these specific T cells. The invention also relates to differential display methods that improve resolution of, and that reduce the frequency of false positives of DNA fragments that are differentially expressed in tumorous, cancerous, or infected tissues versus normal tissues. The invention further relates to the engineering of recombinant viruses as expression vectors for tumor, cancer, or infected cell-specific antigens.

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T CELLS SPECIFIC FOR TARGET ANTIGENS
AND METHODS AND VACCINES BASED THEREON

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1. INTRODUCTION

The present invention relates to novel methods for the identification of antigens recognized by cytotoxic T cells (CTLs) and specific for human tumors, cancers, and infected cells, and the use of such antigens in immunogenic compositions or vaccines to induce regression of tumors, cancers, or infections in mammals, including humans. The invention encompasses methods for induction and isolation of cytotoxic T cells specific for human tumors, cancers or infected cells, and for improved selection of genes that encode the target antigens recognized by these specific T cells. The invention also relates to differential display methods that improve resolution of, and that reduce the frequency of false positives of DNA fragments that are differentially expressed in tumorous, cancerous, or infected tissues versus normal tissues. The invention further relates to the engineering of recombinant viruses as expression vectors for tumor, cancer, or infected cell-specific antigens.

2. BACKGROUND OF THE INVENTION

Current therapies for cancer include surgery, chemotherapy and radiation. The development and use of immunotherapeutic approaches, e.g., tumor targeting using antibody conjugates, "cancer vaccines", etc. is an attractive alternative, but has, to date, met with limited success for a number of reasons. The development of monoclonal antibodies specific for tumor antigens, for example, has proved difficult, in part, because antigens

5 that are recognized by monoclonal antibodies and that are
expressed by tumors and cancer cells are often also
expressed by normal, non-cancerous cells. In addition, the
10 expression of membrane antigens targeted by antibodies is
frequently modulated to permit growth of tumor variants
5 that do not express those antigens at the cell surface. A
cell-mediated immune response may be more effective for
eradication of tumors both because of the different array
15 of effector functions that participate in such responses,
and because T cell-mediated responses target not only
membrane antigens but any tumor-specific intracellular
20 protein that can be processed and presented in association
with major histocompatibility molecules. It is, for this
reason, much more difficult for a tumor to evade T cell-
surveillance by modulating membrane expression.

Immunotherapeutic approaches based on cell-
25 mediated immune responses are likely to be more effective,
15 but antigens that are expressed by tumors and recognized in
cell-mediated immune responses are difficult to identify
and to produce. Development of an effective treatment for
30 cancer through vaccination and subsequent stimulation of
cell-mediated immunity, has remained elusive; the
identification of effective antigens to stimulate cell-
20 mediated responses has been successful only in special
cases, such as melanoma. In melanoma, the cytotoxic T cells
35 (CTLs) that mediate a cellular immune response against
melanoma infiltrate the tumor itself, and such CTLs can be
harvested from the tumor and used to screen for reactivity
40 against other melanoma tumors. Isolation of tumor
25 infiltrating lymphocytes has, however, not been a
successful strategy to recover cytotoxic T cells specific
for most other tumors, in particular the epithelial cell
45 carcinomas that give rise to greater than 80% of human
cancer.

To address the problem of identifying effective
30 antigens for use in vaccination, most previous work has
focused on screening expression libraries with tumor-
50

5 specific CTLs to identify potential tumor antigens. There
are significant limitations to the existing methods of
identifying effective antigens, including the excessively
laborious and inefficient screening process and the
10 considerable difficulty in isolating tumor-specific CTLs
5 for most types of tumors.

2.1. CANCER VACCINES

15 The possibility that altered features of a tumor
cell are recognized by the immune system as non-self and
may induce protective immunity is the basis for attempts to
20 develop cancer vaccines. Whether or not this is a viable
strategy depends on how the features of a transformed cell
are altered. Appreciation of the central role of mutation
in tumor transformation gave rise to the hypothesis that
tumor antigens arise as a result of random mutation in
25 genetically unstable cells. Although random mutations
15 might prove immunogenic, it would be predicted that these
would induce specific immunity unique for each tumor. This
would be unfavorable for development of broadly effective
tumor vaccines. An alternate hypothesis, however, is that
30 a tumor antigen may arise as a result of systematic and
reproducible tissue specific gene deregulation that is
20 associated with the transformation process. This could
give rise to qualitatively or quantitatively different
expression of shared antigens in certain types of tumors
that might be suitable targets for immunotherapy. Early
results, demonstrating that the immunogenicity of some
40 experimental tumors could be traced to random mutations (De
25 Plaen, et al., 1988, Proc. Natl. Acad. Sci. USA 85:
2274-2278; Srivastava, & Old, 1989, Immunol. Today 9: 78),
clearly supported the first hypothesis. There is, however,
45 no a priori reason why random mutation and systematic gene
deregulation could not both give rise to new immunogenic
expression in tumors. Indeed, more recent studies in both
30 experimental tumors (Sahasrabudhe, et al., 1993, J.

5 Immunology 151:6202-6310; Torigoe, et al., 1991, J.
Immunol. 147:3251) and human melanoma (van Der Bruggen, et
al., 1991, Science 254:1643-1647; Brichard, et al., 1993,
J. Exp. Med. 178:489-495; Kawakami, et al., 1994, Proc.
10 Natl. Acad. Sci. USA 91:3515-3519; Boel, et al., 1995,
5 Immunity 2:167-175; Van den Eynde, et al., 1995, J. Exp.
Med. 182: 689-698) have clearly demonstrated expression of
shared tumor antigens encoded by deregulated normal genes.
15 The identification of MAGE-1 and other antigens common to
different human melanoma holds great promise for the future
development of multiple tumor vaccines.

10 In spite of the progress in melanoma, shared
20 antigens recognized by cytotoxic T cells have not been
described for other human tumors. The major challenge is
technological. The most widespread and to date most
successful approach to identify immunogenic molecules
25 uniquely expressed in tumor cells is to screen a cDNA
15 library with tumor-specific CTLs (cytotoxic T lymphocytes).
Application of this strategy has led to identification of
several gene families expressed predominantly in human
30 melanoma. Two major limitations of this approach, however,
are that (1) screening requires labor intensive
transfection of numerous small pools of recombinant DNA
20 into separate target populations in order to assay T cell
35 stimulation by a minor component of some pool; and (2) with
the possible exception of renal cell carcinoma,
tumor-specific CTLs have been very difficult to isolate
from either tumor infiltrating lymphocytes (TIL) or PBL of
40 patients with other types of tumors, especially the
25 epithelial cell carcinomas that comprise greater than 80%
of human tumors. It appears that there may be tissue
specific properties that result in tumor-specific CTLs
being sequestered in melanoma.

45 Direct immunization with tumor-specific gene
products may be essential to elicit an immune response
30 against some shared tumor antigens. It has been argued
50 that, if a tumor expressed strong antigens, it should have

5 been eradicated prior to clinical manifestation. Perhaps
then, tumors express only weak antigens. Immunologists
have long been interested in the issue of what makes an
antigen weak or strong. There have been two major
10 hypotheses. Weak antigens may be poorly processed and fail
5 to be presented effectively to T cells. Alternatively, the
number of T cells in the organism with appropriate
specificity might be inadequate for a vigorous response (a
15 so-called "hole in the repertoire"). Elucidation of the
complex cellular process whereby antigenic peptides
associate with MHC molecules for transport to the cell
20 surface and presentation to T cells has been one of the
triumphs of modern immunology. These experiments have
clearly established that failure of presentation due to
processing defects or competition from other peptides could
render a particular peptide less immunogenic. In contrast,
25 it has, for technical reasons, been more difficult to
15 establish that the frequency of clonal representation in
the T cell repertoire is an important mechanism of low
responsiveness. Recent studies demonstrating that the
30 relationship between immunodominant and cryptic peptides of
a protein antigen change in T cell receptor transgenic mice
suggest, however, that the relative frequency of
20 peptide-specific T cells can, indeed, be a determining
factor in whether a particular peptide is cryptic or
35 dominant in a T cell response. This has encouraging
implications for development of vaccines. With present day
methods, it would be a complex and difficult undertaking to
40 modify the way in which antigenic peptides of a tumor are
25 processed and presented to T cells. The relative frequency
of a specific T cell population can, however, be directly
and effectively increased by prior vaccination. This
45 could, therefore, be the key manipulation required to
render an otherwise cryptic response immunoprotective.

 Another major concern for the development of
30 broadly effective human vaccines is the extreme
polymorphism of HLA class I molecules. Class I

5 MHC:cellular peptide complexes are the target antigens for
specific CD8+ CTLs. The cellular peptides, derived by
degradation of endogenously synthesized proteins, are
translocated into a pre-Golgi compartment where they bind
10 to class I MHC molecules for transport to the cell surface.

5 The CD8 molecule contributes to the avidity of the
interaction between T cell and target by binding to the $\alpha 3$
domain of the class I heavy chain. Since all endogenous
15 proteins turn over, peptides derived from any cytoplasmic
or nuclear protein may bind to an MHC molecule and be
transported for presentation at the cell surface. This
20 allows T cells to survey a much larger representation of
cellular proteins than antibodies which are restricted to
recognize conformational determinants of only those
proteins that are either secreted or integrated at the cell
membrane.

25 The T cell receptor antigen binding site
15 interacts with determinants of both the peptide and the
surrounding MHC. T cell specificity must, therefore, be
defined in terms of an MHC:peptide complex. The
30 specificity of peptide binding to MHC molecules is very
broad and of relatively low affinity in comparison to the
antigen binding sites of specific antibodies. Class
20 I-bound peptides are generally 8-10 residues in length and
accommodate amino acid side chains of restricted diversity
35 at certain key positions that match pockets in the MHC
peptide binding site. These key features of peptides that
bind to a particular MHC molecule constitute a peptide
40 binding motif.

25 Hence, there exists a need for methods to
facilitate the induction and isolation of T cells specific
for human tumors, cancers and infected cells and for
45 methods to efficiently select the genes that encode the
major target antigens recognized by these T cells in the
proper MHC-context.

30

2.2. VACCINIA VECTORS

Poxvirus vectors are used extensively as expression vehicles for protein and antigen, e.g. vaccine antigen, expression in eukaryotic cells. Their ease of cloning and propagation in a variety of host cells has led, in particular, to the widespread use of poxvirus vectors for expression of foreign protein and as delivery vehicles for vaccine antigens (Moss, B. 1991, Science 252:1662-7).

Customarily, the foreign DNA is introduced into the poxvirus genome by homologous recombination. The target protein coding sequence is cloned behind a vaccinia promoter flanked by sequences homologous to a non-essential region in the poxvirus and the plasmid intermediate is recombined into the viral genome by homologous recombination. This methodology works efficiently for relatively small inserts tolerated by prokaryotic hosts. The method becomes less viable in cases requiring large inserts as the frequency of homologous recombination is low and decreases with increasing insert size; in cases requiring construction of labor intensive plasmid intermediates such as in expression library production; and, in cases where the propagation of DNA is not tolerated in bacteria. Hence, there is a need for improved methods of introducing large inserts at high frequency, that do not require such labor intensive genetic engineering.

Alternative methods using direct ligation vectors have been developed to efficiently construct chimeric genomes in situations not readily amenable for homologous recombination (Merchlinsky, M. et al., 1992, Virology 190:522-526; Scheifflinger, F. et al., 1992, Proc. Natl. Acad. Sci. USA. 89:9977-9981). These direct ligation protocols have obviated the need for homologous recombination to generate poxvirus chimeric genomes. In such protocols, the DNA from the genome was digested, ligated to insert DNA *in vitro*, and transfected into cells infected with a helper virus (Merchlinsky, M. et al., 1992,

5 Virology 190:522-526, Scheifflinger, F. et al., 1992, Proc.
Natl. Acad. Sci. USA 89:9977-9981). In one protocol, the
genome was digested at the unique NotI site and a DNA
10 insert containing elements for selection or detection of
the chimeric genomes was ligated to the genomic arms
5 (Scheifflinger, F. et al., 1992, Proc. Natl. Acad. Sci. USA.
89:9977-9981). This direct ligation method was described
for the insertion of foreign DNA into the vaccinia virus
15 genome (Pfleiderer et al., 1995, J. General Virology
76:2957-2962). Alternatively, the vaccinia WR genome was
modified by removing the NotI site in the HindIII F
20 fragment and reintroducing a NotI site proximal to the
thymidine kinase gene such that insertion of a sequence at
this locus disrupts the thymidine kinase gene, allowing
isolation of chimeric genomes via use of drug selection
(Merchlinsky, M. et al., 1992, Virology 190:522-526).
25 The direct ligation vector, vNotI/tk allowed one
15 to efficiently clone and propagate DNA inserts at least 26
kilobase pairs in length (Merchlinsky, M. et al., 1992,
Virology, 190:522-526). Although, large DNA fragments were
30 efficiently cloned into the genome, proteins encoded by the
DNA insert will only be expressed at the low level
corresponding to the thymidine kinase gene, a relatively
20 weakly expressed early class gene in vaccinia. In addition,
35 the DNA will be inserted in both orientations at the NotI
site. Hence, there is a need for more efficient methods of
cloning large DNA fragments into the viral genome with
accompanying high levels of expression of the protein
40 product encoded by the DNA insert. There also exists a
25 need for improved direct ligation vectors. Such vectors
will be more universally useful for the development of
cancer vaccines.

3. SUMMARY OF THE INVENTION

The invention relates to methods for the identification of target antigens recognized by CTLs, and the formulation and use of such antigens in immunogenic compositions or vaccines to induce cell-mediated immunity against target cells, such as tumor cells, that express the target antigens.

Two basic approaches are described for the identification of target antigens. In one approach, CTLs generated against authentic target cells, such as tumor cells, in animals tolerized to non-target (e.g., non-tumorigenic) cellular counterparts are used to screen expression libraries made from target cell-derived (e.g., tumor-derived) DNA, RNA or cDNA to identify clones expressing target antigens. The CTLs generated by the methods described herein are not cross-reactive with normal cells, and thus are better tools for screening. Improved expression libraries are also described.

In a second approach for identifying target antigens, products of genes differentially expressed in target cells, such as tumor cells, are used to immunize animals to generate HLA-restricted CTLs which are evaluated for activity against authentic target cells. Like the first approach, this second strategy could also be particularly useful for identifying epitopes for many human tumor types where it has not been possible to generate tumor-specific CTLs directly from patients. In addition, it may identify cryptic antigens of the intact tumor cell - i.e., tumor cell products which can become immunogenic, if the representation of tumor-specific CTLs is first augmented by vaccination with that tumor cell product. Modified methods for differential display that improve resolution and reduce false positives are described.

In accordance with the present invention, the target cell is a cell to which it is desirable to induce a cell-mediated immune response. Examples of target cells in

5 the body include, but are not limited to, tumor cells,
malignant cells, transformed cells, cells infected with a
virus, fungus, or mycobacteria, or cells subject to any
10 other disease condition which leads to the production of
target antigens.

5 The invention also encompasses the high yield
expression of candidate target antigens, and production of
15 recombinant viruses for vaccine formulation.

3.1. ABBREVIATIONS

10 CTLs - cytotoxic T lymphocytes (T cells)
20 PBL - peripheral blood lymphocytes
RDA - Representational Difference Analysis
TIL - tumor infiltrating lymphocytes

4. DESCRIPTION OF THE FIGURES

25 **Figure 1.** Nucleotide Sequence of p7.5/tk and pEL/tk. The
15 nucleotide sequence of the promoter and beginning of the
thymidine kinase gene for v7.5/tk and vEL/tk.

30 **Figure 2.** Modifications in the nucleotide sequence of the
p7.5/tk vaccinia transfer plasmid. Four new vectors,
20 p7.5/ATG0/tk, p7.5/ATG1/tk, p7.5/ATG3/tk, and p7.5/ATG4/tk
35 have been derived as described in the text from the p7.5/tk
vaccinia transfer plasmid. Each vector includes unique
BamHI, SmaI, PstI, and SalI sites for cloning DNA inserts
that employ either their own endogenous translation
40 initiation site (in vector p7.5/ATG0/tk) or make use of a
25 vector translation initiation site in any one of the three
possible reading frames (p7.5/ATG1/tk, p7.5/ATG3/tk, and
p7.5/ATG4/tk).

45 **Figure 3.** Schematic of the Clontech PCR SELECT™ method of
Representational Difference Analysis. Adapted from
30 information provided by the manufacturer.

5 **Figure 4.** BCA 39 tumor DNA fragments amplified by PCR
following RDA subtraction of B/c.N parental sequences.
Nested primers incorporated into the RDA adapters ligated
10 to BCA 39 tumor cell cDNA were employed for sequential PCR
amplification of the DNA fragments recovered from RDA.
5 Bands are resolved on a 2% Metaphor agarose gel. One
additional low molecular weight band ran off the
15 illustrated gel and was recovered from a shorter
electrophoretic run.

10 **Figure 5.** Hybridization of an RDA fragment of (A) an IAP
pol gene or (B) a fragment of the ubiquitously expressed
20 murine G3PDH cDNA to Northern blots of BCA 39 tumor RNA.
15 micrograms of total RNA was transferred from 1% alkaline
agarose gel to Genescreen nylon membrane by capillary blot
25 in 10X SSC. The Northern blot was first hybridized to the
15 ³²P labeled RDA clone 1 DNA (10³ cpm/ml Stark's hybridization
buffer), then stripped and hybridized with a 350 bp
fragment of G3PDH cDNA.

30 **Figure 6.** RDA clones encoding fragments of IAP gene
elements compared with the full length IAP clone MIA14.
20 One or both terminal regions (filled rectangular box) of
each RDA clone were sequenced to identify homology to
35 subregions of an IAP element. The extent of overlap was
estimated from either the fragment size or, where the
sequence at both termini of a fragment was determined, the
40 known IAP MIA14 sequence spanning the two termini of that
25 fragment. In one case, clone 2.19, the two measures were
not consistent suggesting a deletion in this IAP fragment
in BCA 39 tumor cells.

45 **Figure 7.** Modified Differential Display of cDNA of
parental cell B/c.N and tumors BCA 39, BCA 34, BCA 22, and
30 BCB 13. Fragments of parental and tumor cell cDNA were
50 amplified with one pair of arbitrary decamers, MR_1 (TAC

5 AAC GAG G) and MR_5 (GGA CCA AGT C). For each cell line,
first strand cDNA synthesis was separately primed with MR-1
or MR_5. The two cDNA preparations were then pooled for
10 PCR amplification with both MR_1 and MR_5. A number of
bands can be identified that are associated with all four
5 tumors but not with the immortalized, non-tumorigenic
parental cell line.

15 **Figure 8.** Differential expression in tumor lines of
differential display clone 90. RNase protection assay: 300
picograms of clone 90 antisense probe was hybridized with 5
10 micrograms total RNA prior to RNase digestion and analysis
of protected fragments on 5% denaturing PAGE.

25 **Figure 9.** Gene isolation in solution. Schematic of a
method for selection of longer length cDNA from single
strand circles rescued from a phagemid library. DNA
15 fragments identified through RDA or Modified Differential
Display are employed to select more full length cDNA.

30 **Figure 10.** Restriction Enzyme Analysis of Virus Genomes
Using CHEF Gel. BSC-1 cells were infected at high
20 multiplicity of infection (moi) by vaccinia WR, vEL/tk,
v7.5/tk, or vNotI/tk. After 24 hours the cells were
35 harvested and formed into agarose plugs. The plugs were
equilibrated in the appropriate restriction enzyme buffer
and 1mM PMSF for 16 hours at room temperature, incubated
with restriction enzyme buffer, 100ng/ml Bovine Serum
40 Albumin and 50 units NotI or ApaI for two hours at 37°C
25 (NotI) or room temperature (ApaI) and electrophoresed in a
1.0% agarose gel on a Bio-Rad CHEFII apparatus for 15 hours
45 at 6 V/cm with a switching time of 15 seconds. The
leftmost sample contains lambda DNA, the second sample
contains undigested vaccinia DNA, and the remainder of the
30 samples contain the DNA samples described above each well
digested with ApaI or NotI where vEL refers to vEL/tk and
50

5 v7.5 refers to v7.5/tk. The lower portion of the figure is a schematic map showing the location of the NotI and ApaI sites in each virus.

10 **Figure 11.** Southern Blot Analysis of Viral Genomes p7.5/tk
5 and pEL/tk. The viruses v7.5/tk and vEL/tk were used to infect a well of a 6 well dish of BSC-1 cells at high multiplicity of infection (moi) and after 48 hours the
15 cells were harvested and the DNA was isolated using DNAzol (Gibco). The final DNA product was resuspended in 50 microliters of TE 8.0 and 2.5 microliters were digested
20 with HindIII, HindIII and ApaI, or HindIII and NotI, electrophoresed through a 1.0% agarose gel, and transferred to Nytran (Schleicher and Schuell) using a Turboblotter (Schleicher and Schuell). The samples were probed with
25 p7.5/tk (Figure 11a) or pEL/tk (Figure 11b) labeled with ³²P using Random Primer DNA Labeling Kit (Bio-Rad) in QuickHyb
15 (Stratagene). The lower portion of the figure denotes a map of the HindIII J fragment with the positions of the HindIII, NotI, and ApaI sites illustrated. The leftmost
30 0.5 kilobase fragment has electrophoresed off the bottom of the gel.

20 **Figure 12.** Analysis of v7.5/tk and vEL/tk by PCR. One
35 well of a 6 well dish of BSC-1 cells was infected with v7.5/tk, vEL/tk, vNotI/tk, vpNotI, vNotI/lacZ/tk, or wild type vaccinia WR at high multiplicity of infection (moi) and after 48 hours the cells were harvested, and the DNA
40 was isolated using DNAzol (Gibco). The final DNA product was resuspended in 50 microliters of TE (10mM TrisHCl, pH8.0, 1mM EDTA) and used in a PCR with primers MM407 and
25 MM408. The primers are separated by 518 nucleotides in vaccinia WR and yield a fragment containing the N terminus of the thymidine kinase gene. The products were
45 electrophoresed through a 2% agarose gel. The leftmost
30 sample contains phiX 174 HaeIII digestion products; all

5 others contain the PCR product using primers MM407 and
MM408 with the DNA sample indicated above the well

10 **Figure 13.** Promoter strength of recombinant viruses. The
units of β -glu activity were determined as described by
5 Miller (10) as adapted for 96-well plates. The A_{405} values
were determined on a microplate reader (Dynatech MR3000)
15 and the β -glu activity was determined by comparison to β -
glu (Clontech) standards analyzed in the same assay.

10 **Figure 14.** Plaque assay on vEL/tk. Ten-fold dilutions of
vEL/tk were incubated with Hutk⁻ cells (top to bottom) for
20 one hour at 37°C in 1ml of E-MEM (Gibco) with 10% Fetal
Bovine Serum for one hour, the media was replaced with 3ml
of E-MEM with 5% methyl cellulose (Sigma M-0387), 5% Fetal
25 Bovine Serum and HAT supplement (Gibco), 25 or 125mM
bromodeoxyuridine, or no drug, incubated for 48 hours at
15 37°C, and stained with 0.5% Crystal Violet (Sigma C 0775),
20% ethanol, 7.5% formaldehyde.

30 5. DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to methods for the
20 identification of target antigens recognized by CTLs, and
the use of such antigens in immunogenic compositions or
35 vaccines to induce a cell-mediated immune response against
cells which express the target antigens.

In one embodiment of the invention, tumor-
specific CTLs generated in animals are used to screen
40 expression libraries generated from tumor cell DNA, RNA or
25 cDNA to identify reactive target antigens. To this end,
animals tolerized with a non-tumorigenic human cell line
are immunized with tumor cells derived from the non-
45 tumorigenic cell line. The resulting CTLs, which are
tumor-specific and not cross-reactive with normal cells,
30 can be used to screen expression libraries constructed from
tumor-cell derived DNA, RNA or cDNA. Clones so identified

5 in the library encode target antigens which are candidates
for the immunogenic compositions and vaccines of the
invention. Improved and modified vaccinia virus vectors
10 for efficient construction of such DNA libraries using a
"trimolecular recombination" approach are described to
5 improve screening efficiency.

It is a preferred embodiment of the invention to
tolerize animals, such as normal or transgenic mice, with
15 normal human cells prior to immunizing with human tumor
cells. Tolerance induction is preferred because the
animal's immune response would otherwise be dominated by
20 specificity for a large number of broadly expressed human
proteins that are not specifically associated with tumor
transformation. In a particularly preferred embodiment,
and to enhance the efficiency of this approach, it is
convenient to work with human tumors that are derived from
25 an immortalized, non-tumorigenic human cell line by in
15 vitro carcinogenesis or oncogene transformation. This
provides a ready source of the normal control cells for an
extended tolerization protocol in both neonatal and adult
30 mice. For example, CTLs generated by this approach (see
Section 7 below) can be employed in a selection procedure
20 (such as that described in Section 8 below) to isolate
recombinant clones that encode the target antigens from a
35 tumor cDNA library, for example, such as that constructed
in vaccinia virus by tri-molecular recombination (see
Section 6 below).

In another embodiment of the invention, the
40 products of genes that are differentially expressed in
25 tumor cells are used to generate HLA-restricted CTLs which
are evaluated for activity against authentic tumor cells.
It is particularly preferred if methods such as
45 Representational Difference Analysis (RDA) and differential
display are employed to identify gene fragments that are
differentially expressed in tumor versus normal cells.
30 Conveniently, if it is determined that these gene products

5 are broadly expressed in other related tumors (see, for
example, Sections 10 and 11 below), they may be used to
select longer clones from the library (see, for example,
10 Section 9.5) which may be tested for the ability to induce
a tumor-specific immune response in, for example, human CD8
5 and HLA transgenic mice (see, for example, Section 12).
Gene products which generate tumor-specific cell mediated
immunity are also candidates for the immunogenic
15 compositions and vaccines of the invention. Improved
methods for differential display are described that enhance
screening efficiency by reducing false positives, and
20 enhance the efficiency for isolating full length cDNAs.

The antigens identified using any of the
foregoing strategies can be produced in quantity by
recombinant DNA methods and formulated with an adjuvant
that promotes a cell-mediated immune response. Preferably,
25 the DNA encoding the target antigen is engineered into a
15 recombinant virus that can be used to vaccinate animal
hosts, including humans. In this regard, improved direct
ligation vaccinia vectors are described that can be used to
30 generate vaccines.

Another therapeutic strategy of the invention is
to design vaccines that target a small set of HLA class I
20 molecules which are expressed at elevated frequencies
35 across ethnic populations. Extensive characterization of
peptide binding motifs of different human class I MHC
molecules has suggested that there are four major subtypes
of HLA-A and HLA-B alleles (Sidney, J., et al., 1996,
40 Immunol. Today 17:261-266) such that many peptides will
25 bind to multiple members of a single group. The present
invention also provides methods to target vaccines for
patients based on their membership in a class I MHC group.
45 In specific embodiments, class I MHC subtypes A2, A3, B7
and B44 are targeted. Each group has an average
representation across ethnic populations of between 40% and
30 50%. It is estimated that the combination of all four
50 groups (which include 50% to 60% of all known HLA-A and

5 HLA-B alleles) covers 95% of the human population. In a
specific embodiment, HLA-A2.1, the most frequently
expressed HLA allele in human populations (Caucasian 43%,
10 Black 20%, Chinese 25%) and the dominant member of the A2
subtype, is targeted.

5 Although the methods of the invention described
are used to identify reactive target antigens in tumor
cells, the methods may also be used to identify target
15 antigens in other target cells against which it is
desirable to induce cell-mediated immunity. For example,
the differential immunogenicity methods of the invention
10 can be applied to identify immunogenic molecules of cells
infected with virus, fungus or mycobacteria by tolerization
of mice with uninfected cells followed by immunization with
infected cells at different times after infection. The
isolated CTLs can be employed to select recombinants that
25 encode target antigens in a plasmid or viral expression
15 library. An expression library can be constructed with
cDNA isolated from the infected cell in a vaccinia virus
vector using tri-molecular recombination.

30 A particular advantage of this approach is that
it will identify potential antigens expressed not only by
the pathogen but also by the host cell whose gene
20 expression is altered as a result of infection. Since many
35 pathogens elude immune surveillance by frequent
reproduction and mutation, it may be of considerable value
to develop a vaccine that targets host gene products that
are not likely to be subject to mutation.

40 The differential gene expression strategies of the
25 present invention may also be applied to identify
immunogenic molecules of cells infected with virus, fungus
or mycobacteria. More stable and/or previously
45 unidentified antigens encoded by genes of either pathogen
or host, including those which might remain cryptic without
prior specific vaccination, may be identified.

30 Pathogens include, but are not limited to:

5 viral pathogens, such as human immunodeficiency virus,
Epstein BArr virus, hepatitis virus, herpes virus, human
papillomavirus, cytomegalovirus, respiratory syncytial
10 virus; fungal pathogens, such as Candida albicans,
pneumocystis carinii; and mycobacterial pathogens, such as
5 M. tuberculosis, M. avium.

The following details and examples mention
primarily target antigens in tumor cells. As will be
15 appreciated from the foregoing, the methods of the
invention may be adapted to identify target antigens in
other target cells, such as virally infected cells, and may
10 be useful in developing vaccines.

5.1. IDENTIFYING TARGET ANTIGENS FOR USE IN VACCINES

The subsections below describe two strategies
25 that can be used to identify target antigens or epitopes
15 that are candidates for use in immunogenic formulations or
vaccines. The two strategies described herein may be
applied to identify target epitopes which include, but are
30 not limited to, tumor specific, epitopes specific to a cell
infected with a virus, fungus or mycobacteria, and/or
epitopes specific to an autoimmune disease.
20

5.1.1. INDUCTION OF CYTOTOXIC T LYMPHOCYTES SPECIFIC FOR HUMAN TUMORS AND THEIR USE TO SELECT DNA RECOMBINANTS THAT 35 ENCODE TARGET EPITOPES

40 In this embodiment of the invention, cytotoxic T
25 cells specific for human tumors are induced in animals
which have been tolerized with a non-tumorigenic,
immortalized normal human cell line that does not express
45 costimulator activity. These animals are subsequently
immunized with costimulator transfected (e.g., B7
transfected) tumor cells derived by in vitro mutagenesis or
30 oncogene transformation from that same normal immortalized

5 human cell line. An alternative source of matched normal
and tumor cell pairs that could be employed in this same
fashion is to derive normal and tumor cell lines from
10 different tissue samples of the same patient. For purposes
of immunization, costimulator activity could also be
5 introduced in these tumor cells by transfection with murine
B7. This immunization regimen gives rise to tumor-specific
CTL that are not crossreactive on the homologous normal
15 cells. The primary purpose of inducing tumor-specific CTL
is that they can be employed, as described below, to select
for clones of recombinant tumor DNA that encode the target
20 antigen. Such antigens, because they are differentially
immunogenic in tumor as compared to normal cells, are
candidates for immunogenic formulations or vaccines.
Mammals of different species, most commonly diverse strains
of inbred mice, can be employed for this purpose. Whether
25 a particular formulation or vaccine is immunogenic in any
particular individual will depend on whether specific
15 peptides derived from that antigen can be processed and
presented in association with the particular MHC molecules
expressed by that individual. To narrow the focus of this
30 selection process to antigens from which peptides can be
derived that associate with a particular human HLA
20 molecule, it is possible, as described in Section 7, to
derive directly HLA restricted CTL from HLA and human CD8
35 transgenic mice. Alternatively, differentially immunogenic
molecules of the human tumor can be initially identified
employing tumor-specific CTL restricted to any animal MHC.
40 Antigens so identified can subsequently be characterized
25 for the ability to be processed and presented in
association with different human HLA types by primary in
vitro stimulation of human peripheral blood lymphocytes
45 (PBL), or, as described in Section 12, by immunization of
HLA and human CD8 transgenic mice. The HLA transgene
30 permits selection of a high affinity, HLA- restricted T
cell repertoire in the mouse thymus. In addition, a human

5 CD8 transgene is most preferable because murine CD8 does not interact efficiently with human class I MHC.

10 The method to determine differential immunogenicity can be carried out in normal mice if genes encoding mouse MHC molecules are introduced into the human
5 cell lines by transfection (Kriegler, M., 1991, Gene transfer and expression: A laboratory manual, W.H. Freeman and Co., N.Y.). Alternatively, antigens of the human cell
15 lines may be re-presented by murine professional antigen presenting cells *in vivo* (Huang, et al., 1994, Science, 264:961-965) and *in vitro* (Inaba, et al., 1992, J. Exp.
20 Med. 176:1702; Inaba, et al., 1993, J. Exp. Med. 178:479-488). To induce T cell tolerance during re-presentation of human antigens by murine dendritic cells it may be necessary to block costimulator activity with anti-B7.1 and
25 anti-B7.2 antibodies. Specificity of the CTL generated in this way may be determined by comparing lysis of human
15 tumor and normal target cells that have been transfected with HLA class I or that have been infected with HLA class I or that have been infected with HLA class I recombinant
30 vaccinia virus.

20 Since immunogenicity of antigen in any individual depends on whether peptides derived from the antigen can be presented to T cells in association with MHC molecules of
35 that particular individual, it may be separately determined by immunization of human volunteers or of human CD8 and HLA transgenic mice, which human HLA molecules are able to present peptides of any identified antigen. The two issues
40 of immunogenicity and HLA associated presentation can be
25 addressed simultaneously if HLA transgenic mice rather than normal mice are employed in the initial immunization.

45 The construction of transgenic mice is well known in the art and is described, for example, in Manipulating the Mouse Embryo: A laboratory Manual, Hogan, et al., Cold Spring Harbor Press, second edition, 1994. Human CD8
30 transgenic mice may be constructed by the method of LaFace,

5 et al., J. Exp. Med. 182: 1315-25 (1995). Construction of
new lines of transgenic mice expressing the human CD8alpha
and CD8beta subunits may be made by insertion of the
10 corresponding human cDNA into a human CD2 minigene based
vector for T cell-specific expression in transgenic mice
5 (Zhumabekov, et al., J. Immunol. Methods 185:133-140
(1995)). HLA class I transgenic mice may be constructed by
the methods of Chamberlain, et al., Proc. Natl. Acad. Sci.
15 USA 85:7690-7694 (1988) or Bernhard, et al., J. Exp. Med.
168: 1157-62 (1988) or Vitiello, et al., J. Exp. Med. 173:
1007-1015 (1991) or Barra, et al., J. Immunol. 150: 3681-9
20 (1993).

Construction of additional HLA class I transgenic
mice may be achieved by construction of an H-2Kb cassette
that includes 2 kb of upstream regulatory region together
25 with the first two introns previously implicated in gene
regulation (Kralova, et al., 1992, EMBO J. 11: 4591-4600).
15 Endogenous translational start sites are eliminated from
this region and restriction sites for insertion of HLA cDNA
are introduced into the third exon followed by a polyA
30 addition site. By including an additional 3kb of genomic
H-2Kb sequence at the 3' end of this construct, the class I
gene can be targeted for homologous recombination at the H-
20 2Kb locus in embryonic stem cells. This has the advantage
35 that the transgene is likely to be expressed at a defined
locus known to be compatible with murine class I expression
and that these mice are likely to be deficient for possible
40 competition by H-2Kb expression at the cell membrane. It
is believed that this will give relatively reproducible
25 expression of diverse human HLA class I cDNA introduced in
the same construct.

Most preferably, the tumor cell lines are a panel
45 of tumor cell lines that are all derived from a single
immortalized, non-tumorigenic cell line. Non-tumorigenic
cells are most preferable for inducing tolerance to the
30 large number of normal human proteins that are also
50 expressed in tumor cells.

5

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Preferably, screening is performed on such a panel of tumor cell lines, independently derived from the same normal cells by diverse carcinogens or oncogene transformation. Screening of such a panel of tumor cell lines makes it possible to filter out antigenic changes that are carcinogen specific or that may arise by random genetic drift during in vitro propagation of a tumor cell line.

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The tumor-specific CTLs generated as described above can be used to screen expression libraries prepared from the target tumor cells in order to identify clones encoding the target epitope. DNA libraries constructed in a viral vector infectious for mammalian cells as described herein can be employed for the efficient selection of specific recombinants by CTLs. Major advantages of these infectious viral vectors are 1) the ease and efficiency with which recombinants can be introduced and expressed in mammalian cells, and 2) efficient processing and presentation of recombinant gene products in association with MHC molecules of the infected cell. At a low multiplicity of infection (m.o.i.), many target cells will express a single recombinant which is amplified within a few hours during the natural course of infection.

35

40

In one embodiment of the invention, a representative DNA library is constructed in vaccinia virus. Preferably, a tri-molecular recombination method employing modified vaccinia virus vectors and related transfer plasmids is used to construct the representative DNA library in vaccinia virus. This method generates close to 100% recombinant vaccinia virus (see Section 6, Section 6.2 and 6.3).

45

50

In a preferred embodiment (see also Section 14, Section 14.1.1), a vaccinia virus transfer plasmid pJ/K, a pUC 13 derived plasmid with a vaccinia virus thymidine kinase gene containing an in-frame Not I site, is further modified to incorporate one of two strong vaccinia virus

5 promoters, e.g., either a 7.5K vaccinia virus promoter or a
strong synthetic early/late (E/L) promoter, followed by Not
I and Apa I restriction sites. The Apa I site is
10 preferably preceded by a strong translational initiation
sequence including the ATG codon. This modification is
5 preferably introduced within the vaccinia virus thymidine
kinase (*tk*) gene so that it is flanked by regulatory and
15 coding sequences of the viral *tk* gene. Each of the two
modifications within the *tk* gene of a plasmid vector may be
transferred by homologous recombination in the flanking *tk*
20 sequences into the genome of the Vaccinia Virus WR strain
derived vNotI vector to generate two new viral vectors.
Importantly, following Not I and Apa I restriction
endonuclease digestion of these two viral vectors, two
25 large viral DNA fragments can be isolated each including a
separate non-homologous segment of the vaccinia *tk* gene and
15 together comprising all the genes required for assembly of
infectious viral particles.

30 In one embodiment, such modifications are
introduced in the Modified Virus Ankara (MVA) strain of
vaccinia, which is replication deficient in mammalian cells
(Meyer, et al., 1991. J. Gen. Virol. 72:1031-1038).

20 In a preferred embodiment, the following method
35 is used to enrich for, and select for those cells infected
with the recombinant viruses that express the target
epitopes of specific cytotoxic T cells. An adherent
monolayer of cells is infected with a recombinant viral
40 library, e.g. a vaccinia recombinant viral library, at
25 m.o.i. less than or equal to 1. It is important that these
cells do not themselves express the target epitopes
recognized by specific CTLs but that these epitopes are
45 represented in the viral library. In addition, for
selection by CTLs, the infected cells must express an
appropriate MHC molecule that can associate with and
30 present the target peptide to T cells.

5 After 12 hours infection with recombinant virus,
the monolayer is washed to remove any non-adherent cells.
CTLs of defined specificity are added for 30 min. During
10 this time, some of the adherent cells infected with a
recombinant particle that leads to expression of the target
5 epitope will interact with a specific CTL and undergo a
lytic event. Cells that undergo a lytic event are released
15 from the monolayer and can be harvested in the floating
cell population. The above-described protocol is repeated
for preferably five or more cycles, to increase the level
of enrichment obtained by this procedure.

20 5.1.2. SCREENING CYTOTOXIC LYMPHOCYTES
GENERATED AGAINST PRODUCTS OF
GENES DIFFERENTIALLY EXPRESSED
IN TUMOR CELLS FOR ACTIVITY
25 AGAINST AUTHENTIC TUMOR CELLS

15 In this embodiment of the invention, the products
of genes that are differentially expressed in a tumor are
used to generate HLA-restricted CTLs (e.g., by immunization
30 of transgenic animals or *in vitro* stimulation of human PBL
with antigen presenting cells that express the appropriate
MHC). The CTLs so generated are assayed for activity
20 against authentic tumor cells in order to identify the
35 differentially expressed gene which encodes the effective
target epitope.

In essence, this approach to identify tumor-
specific antigens is the reverse of the strategy described
40 in the preceding section. Rather than isolating CTLs
25 generated against authentic tumor cells to screen
expression libraries of tumor-specific cDNA, the tumor-
specific cDNA or gene products (i.e., the product of genes
45 differentially expressed in tumors) are used to generate
CTLs which are then screened using authentic tumor. This
strategy is quite advantageously used to identify target
30 epitopes for many human tumor types where it has not been
50 possible to generate tumor-specific CTL directly from

5 patients. This strategy provides an additional advantage
in that cryptic tumor antigens can be identified. Rather
than only assaying for what is immunogenic on a tumor cell,
10 this embodiment of the invention allows for the evaluation
and assessment of tumor cell products that can become
5 immunogenic if the representation of tumor-specific T cells
is first augmented by vaccination.

15 Differentially expressed genes derived from the
tumor can be identified using standard techniques well
known to those skilled in the art (e.g., see Liang &
Pardee, 1992, Science 257:967-971, which is incorporated by
20 reference herein in its entirety). Preferably, the
improved differential display methods described in Sections
9.2 and 9.3, infra, may be used to reduce false positives
and enhance the efficiency for isolating full length cDNAs
corresponding to the identified DNA fragments. Each
25 differentially expressed gene product is potentially
15 immunogenic, and may be represented as a low-abundance or
high abundance transcript.

30 In order to identify the differentially expressed
gene products that might be candidates for tumor
immunotherapy, it is necessary to have a means of
delivering the product for immunization in an environment
20 in which T cell responses to peptides associated with human
35 HLA can be induced. To this end, the differentially
expressed cDNA is incorporated into an expression vector,
preferably a viral vector (such as the vaccinia vectors
described herein) so that quantities of the gene product
adequate for immunization are produced. Immunization can
40 25 be accomplished using the recombinantly expressed gene
product formulated in a subunit vaccine (e.g., mixed with a
suitable adjuvant that can promote a cell mediated immune
45 response). Preferably a recombinant viral expression
vector, such as vaccinia, can be used to immunize (Benneck
& Yewdell, 1990, Current Topics In Microbiol. and Immunol.
30 163:153-178). Most preferably, transgenic mice are
50 employed which express a human class I MHC molecule, so

5 that HLA-restricted murine cytotoxic T cells specific for
the gene product can be induced and isolated (Shirai, M.,
et al., 1995, J. Immunol. 154:2733-42; Wentworth et al.,
10 1996, Eur. J. of Immunol. 26:97-101). Alternatively, human
PBL are stimulated *in vitro* with antigen presenting cells
5 that express homologous HLA.

The significance of HLA compatibility is that T
15 cells recognize peptides that bind to, and are transported
to the surface of antigen presenting cells in association
with major histocompatibility molecules. T cells of HLA
transgenic mice are, therefore, primed to recognize a
20 specific peptide in association with the expressed human
HLA and crossreactivity with human tumor cells depends on
expression of that same tumor peptide in association with
the same HLA molecule.

The CTLs induced by the immunization can be
25 tested for cross reactivity on HLA compatible tumors that
15 express the corresponding mRNA. The CTLs can be assayed
for their ability to kill authentic tumor cells *in vitro* or
30 *in vivo*. To this end, assays described in Section 7 can be
used, or other similar assays for determining tumor cell
specificity and killing which are well known to those
20 skilled in the art.

35 Using this approach, target epitopes which are
particularly good candidates for tumor immunotherapy in
human patients are identified as those which meet the
following criteria: (a) the gene is differentially
40 expressed in multiple human tumors; (b) the gene products
25 are immunogenic in association with HLA; and (c) the
specific CTLs induced are cross reactive on human tumor
cells.

5.2. VACCINE FORMULATIONS

The present invention encompasses the expression of the identified target epitope in either eucaryotic or procaryotic recombinant expression vectors; and the formulation of the identified epitope as immunogenic and/or antigenic compositions. In accordance with the present invention, the recombinantly expressed target epitope may be expressed, purified and formulated as a subunit vaccine. The identified target epitope may also be constructed into viral vectors for use in vaccines. In this regard, either a live recombinant viral vaccine, an inactivated recombinant viral vaccine, or a killed recombinant viral vaccine can be formulated.

5.2.1. EXPRESSION OF THE TARGET EPITOPE
IN PROCARYOTIC AND EUCARYOTIC
EXPRESSION SYSTEMS

The present invention encompasses expression systems, both eucaryotic and procaryotic expression vectors, which may be used to express the identified target epitope. The identified epitope may be expressed in both truncated or full-length forms of the epitope, in particular for the formation of subunit vaccines.

The present invention encompasses the expression of nucleotide sequences encoding the identified epitopes and immunologically equivalent fragments. Such immunologically equivalent fragments may be identified by making analogs of the nucleotide sequence encoding the identified epitopes that are truncated at the 5' and/or 3' ends of the sequence and/or have one or more internal deletions, expressing the analog nucleotide sequences, and determining whether the resulting fragments immunologically are recognized by the epitope specific CTLs and induce a cell-mediated immune response.

The invention encompasses the DNA expression vectors that contain any of the foregoing coding sequences

operatively associated with a regulatory element that directs expression of the coding sequences and genetically engineered host cells that contain any of the foregoing coding sequences operatively associated with a regulatory element that directs the expression of the coding sequences in the host cell. As used herein, regulatory elements include but are not limited to, inducible and non-inducible promoters, enhancers, operators and other elements known to those skilled in the art that drive and regulate expression.

The target epitope gene products or peptide fragments thereof, may be produced by recombinant DNA technology using techniques well known in the art. Thus, methods for preparing the epitope gene polypeptides and peptides of the invention by expressing nucleic acid containing epitope gene sequences are described herein. Methods which are well known to those skilled in the art can be used to construct expression vectors containing epitope gene product coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. See, for example, the techniques described in Sambrook et al., 1989, supra, and Ausubel et al., 1989, supra. Alternatively, RNA capable of encoding glycoprotein epitope gene product sequences may be chemically synthesized using, for example, synthesizers. See, for example, the techniques described in "Oligonucleotide Synthesis", 1984, Gait, M.J. ed., IRL Press, Oxford, which is incorporated by reference herein in its entirety.

The invention also encompasses nucleotide sequences that encode peptide fragments of the identified epitope gene products. For example, polypeptides or peptides corresponding to the extracellular domain of the selected epitope may be useful as "soluble" protein which would facilitate secretion, particularly useful in the

5 production of subunit vaccines. The selected epitope gene
product or peptide fragments thereof, can be linked to a
heterologous epitope that is recognized by a commercially
10 available antibody is also included in the invention. A
durable fusion protein may also be engineered; i.e., a
5 fusion protein which has a cleavage site located between
the selected epitope sequence and the heterologous protein
sequence, so that the selected epitope can be cleaved away
15 from the heterologous moiety. For example, a collagenase
cleavage recognition consensus sequence may be engineered
between the selected epitope protein or peptide and the
10 heterologous peptide or protein. The epitopic domain can
be released from this fusion protein by treatment with
collagenase. In a preferred embodiment of the invention, a
20 fusion protein of glutathione-S-transferase and the
selected epitope protein may be engineered.

25 The selected epitope proteins of the present
15 invention for use in vaccine preparations, in particular
subunit vaccine preparations, are substantially pure or
homogeneous. The protein is considered substantially pure
or homogeneous when at least 60 to 75% of the sample
30 exhibits a single polypeptide sequence. A substantially
pure protein will preferably comprise 60 to 90% of a
20 protein sample, more preferably about 95% and most
preferably 99%. Methods which are well known to those
35 skilled in the art can be used to determine protein purity
or homogeneity, such as polyacrylamide gel electrophoresis
of a sample, followed by visualizing a single polypeptide
40 band on a staining gel. Higher resolution may be
25 determined using HPLC or other similar methods well known
in the art.

45 The present invention encompasses polypeptides
which are typically purified from host cells expressing
recombinant nucleotide sequences encoding these proteins.
Such protein purification can be accomplished by a variety
30 of methods well known in the art. In a preferred
embodiment, the epitope protein of the present invention is
50

5 expressed as a fusion protein with glutathione-S-
transferase. The resulting recombinant fusion proteins
purified by affinity chromatography and the epitope protein
10 domain is cleaved away from the heterologous moiety
resulting in a substantially pure protein sample. Other
5 methods known to those skilled in the art may be used; see
for example, the techniques described in "Methods In
Enzymology", 1990, Academic Press, Inc., San Diego,
15 "Protein Purification: Principles and Practice", 1982,
Springer-Verlag, New York, which are incorporated by
reference herein in their entirety.

10

20 5.2.1.1. EUCARYOTIC AND PROCARYOTIC EXPRESSION

VECTORS

The present invention encompasses expression
systems, both eucaryotic and procaryotic expression
25 vectors, which may be used to express the selected epitope.
15 A variety of host-expression vector systems may be utilized
to express the selected target epitope gene of the
invention. Such host-expression systems represent vehicles
30 by which the coding sequences of interest may be produced
and subsequently purified, but also represent cells which
may, when transformed or transfected with the appropriate
20 nucleotide coding sequences, exhibit the selected epitope
gene product of the invention in situ. These include but
35 are not limited to microorganisms such as bacteria (e.g.,
E. coli, B. subtilis) transformed with recombinant
bacteriophage DNA, plasmid DNA or cosmid DNA expression
40 vectors containing selected epitope gene product coding
25 sequences; yeast (e.g., Saccharomyces, Pichia) transformed
with recombinant yeast expression vectors containing the
selected epitope gene product coding sequences; insect cell
45 systems infected with recombinant virus expression vectors
(e.g., baculovirus) containing the selected epitope gene
30 product coding sequences; plant cell systems infected with
recombinant virus expression vectors (e.g., cauliflower

50

- 30 -

SUBSTITUTE SHEET (RULE 26)

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5 mosaic virus, CaMV; tobacco mosaic virus, TMV) or
transformed with recombinant plasmid expression vectors
(e.g., Ti plasmid) containing selected epitope gene product
coding sequences; or mammalian cell systems (e.g., COS,
10 CHO, BHK, 293, 3T3) harboring recombinant expression
5 constructs containing promoters derived from the genome of
mammalian cells (e.g., metallothionein promoter) or from
mammalian viruses (e.g., the adenovirus late promoter; the
15 vaccinia virus 7.5K promoter).

5.2.1.2. HOST CELLS

10 The present invention encompasses the expression
of the selected epitope in animal and insect cell lines.
In a preferred embodiment of the present invention, the
selected epitope is expressed in a baculovirus vector in an
insect cell line to produce an unglycosylated antigen. In
25 another preferred embodiment of the invention, the selected
15 epitope is expressed in a stably transfected mammalian host
cell, e.g., T lymphocyte cell line to produce a
glycosylated antigen. The selected epitopes which are
expressed recombinantly by these cell lines may be
30 formulated as subunit vaccines.

A host cell strain may be chosen which modulates
20 the expression of the inserted sequences, or modifies and
processes the gene product in the specific fashion desired.
Such modifications (e.g., glycosylation) and processing
(e.g. cleavage) of protein products may be important for
the function of the protein. Different host cells have
40 characteristic and specific mechanisms for the post-
25 translational processing and modification of proteins and
gene products. Appropriate cell lines or host systems can
be chosen to ensure the correct modification of the foreign
protein expressed. To this end, eucaryotic host cells
45 which possess the cellular machinery for proper processing
of the primary transcript, glycosylation, and
30 phosphorylation of the gene product may be used. Such

5 mammalian host cells include but are not limited to CHO,
VERO, BHK, HeLa, COS, MDCK, 293, 3T3 and WI38 cell lines.

10 For long term, high-yield production of
recombinant proteins, stable expression is preferred. For
example, cell lines which stably express the selected
5 target epitope may be engineered. Rather than using
expression vectors which contain viral origins of
replication, host cells can be transformed with DNA
15 controlled by appropriate expression control elements
(e.g., promoter, enhancer, sequences, transcription
terminators, polyadenylation sites, etc.), and a selectable
20 marker. Following the introduction of the foreign DNA,
engineered cells may be allowed to grow for 1-2 days in an
enriched media, and then are switched to a selective media.
The selectable marker in the recombinant plasmid confers
resistance to the selection and allows cells to stably
25 integrate the plasmid into their chromosomes and grow to
form foci which in turn can be cloned and expanded into
cell lines. This method may advantageously be used to
engineer cell lines. This method may advantageously be
30 used to engineer cell lines which express the selected
epitope gene products. Such cell lines would be
particularly useful in screening and evaluation of
20 compounds that affect the endogenous activity of the
selected epitope gene product.

35 A number of selection systems may be used,
including but not limited to the herpes simplex virus
thymidine kinase (Wigler, et al., 1977, Cell 11:223),
40 hypoxanthine-guanine phosphoribosyltransferase (Szybalska &
25 Szybalski, 1962, Proc. Natl. Acad. Sci. USA 48:2026), and
adenine phosphoribosyltransferase (Lowy, et al., 1980, Cell
22:817) genes can be employed in tk⁻, hgp⁺ or ap⁺ cells,
45 respectively. Also, antimetabolite resistance can be used
as the basis of selection for the following genes: dhfr,
which confers resistance to methotrexate (Wigler, et al.,
30 1980, Natl. Acad. Sci. USA 77:3567; O'Hare, et al., 1981,
Proc. Natl. Acad. Sci. USA 78:1527); gpt, which confers

5 resistance to mycophenolic acid (Mulligan & Berg, 1981,
Proc. Natl. Acad. Sci. USA 78:2072); neo, which confers
10 resistance to the aminoglycoside G-418 (Colberre-Garapin,
et al., 1981, J. Mol. Biol. 150:1); and hygro, which
confers resistance to hygromycin (Santerre, et al., 1984,
5 Gene 30:147).

Alternatively, any fusion protein may be readily
15 purified by utilizing an antibody specific for the fusion
protein being expressed. For example, a system described
by Janknecht et al. allows for the ready purification of
non-denatured fusion proteins expressed in human cell lines
20 (Janknecht, et al., 1991, Proc. Natl. Acad. Sci. USA 88:
8972-8976). In this system, the gene of interest is
subcloned into a vaccinia recombination plasmid such that
the gene's open reading frame is translationally fused to
an amino-terminal tag consisting of six histidine residues.
25 Extracts from cells infected with recombinant vaccinia
virus are loaded onto Ni²⁺-nitriloacetic acid-agarose
columns and histidine-tagged proteins are selectively
eluted with imidazole-containing buffers.

5.2.2. EXPRESSION OF TARGET EPITOPE IN RECOMBINANT VIRAL VACCINES

20 In another embodiment of the present invention,
35 either a live recombinant viral vaccine or an inactivated
recombinant viral vaccine expressing the selected target
epitope can be engineered. A live vaccine may be preferred
because multiplication in the host leads to a prolonged
40 stimulus of similar kind and magnitude to that occurring in
25 natural infections, and therefore, confers substantial,
long-lasting immunity. Production of such live
recombinant virus vaccine formulations may be accomplished
45 using conventional methods involving propagation of the
virus in cell culture or in the allantois of the chick
embryo followed by purification.
30

5 In this regard, a variety of viruses may be
genetically engineered to express the selected epitope.
For vaccine purposes, it may be required that the
10 recombinant viruses display attenuation characteristics.
Current live virus vaccine candidates for use in humans are
5 either cold adapted, temperature sensitive, or attenuated.
The introduction of appropriate mutations (e.g., deletions)
into the templates used for transfection may provide the
15 novel viruses with attenuation characteristics. For
example, specific multiple missense mutations that are
associated with temperature sensitivity or cold adaptation
20 can be made into deletion mutations and/or multiple
mutations can be introduced into individual viral genes.
These mutants should be more stable than the cold or
temperature sensitive mutants containing single point
25 mutations and reversion frequencies should be extremely
low. Alternatively, recombinant viruses with "suicide"
15 characteristics may be constructed. Such viruses go
through only one or a few rounds of replication in the
host.

30 For purposes of the invention, any virus may be
used in accordance with the present invention which: (a)
displays an attenuated phenotype or may be engineered to
20 display attenuated characteristics; (b) displays a tropism
for mammals, in particular humans, or may be engineered to
35 display such a tropism; and (c) may be engineered to
express the selected target epitope of the present
invention.

40 Vaccinia viral vectors may be used in accordance
25 with the present invention, as large fragments of DNA are
easily cloned into its genome and recombinant attenuated
vaccinia variants have been described (Meyer, et al., 1991,
45 J. Gen. Virol. 72:1031-1038). Orthomyxoviruses, including
influenza; Paramyxoviruses, including respiratory syncytial
virus and Sendai virus; and Rhabdoviruses may be engineered
30 to express mutations which result in attenuated phenotypes
(see U.S. Patent Serial No. 5,578,473, issued November 26,
50

5 1996). These viral genomes may also be engineered to
express foreign nucleotide sequences, such as the selected
epitopes of the present invention (see U.S. Patent Serial
10 No. 5,166,057, issued November 24, 1992, incorporated
herein by reference in its entirety). Reverse genetic
5 techniques can be applied to manipulate negative and
positive strand RNA viral genomes to introduce mutations
which result in attenuated phenotypes, as demonstrated in
15 influenza virus, Herpes Simplex virus, cytomegalovirus and
Epstein-Barr virus, Sindbis virus and poliovirus (see
Palese et al., 1996, Proc. Natl. Acad. Sci. USA 93:11354-
20 11358). These techniques may also be utilized to introduce
foreign DNA, i.e., the selected target epitopes, to create
recombinant viral vectors to be used as vaccines in
accordance with the present invention. In addition,
25 attenuated adenoviruses and retroviruses may be engineered
to express the target epitope. Therefore, a wide variety
15 of viruses may be engineered to design the vaccines of the
present invention, however, by way of example, and not by
limitation, recombinant attenuated vaccinia vectors
30 expressing the selected target epitope for use as vaccines
are described herein.

In one embodiment, a recombinant modified
20 vaccinia variant, Modified Virus Ankara (MVA) is used in a
vaccine formulation. This modified virus has been passaged
35 for 500 cycles in avian cells and is unable to undergo a
full infectious cycle in mammalian cells (Meyer, et al.,
1991, J. Gen. Virol. 72:1031-1038). When used as a
40 vaccine, the recombinant virus goes through a single
25 replication cycle and induces a sufficient level of immune
response but does not go further in the human host and
cause disease. Recombinant viruses lacking one or more of
45 essential vaccinia virus genes are not able to undergo
successive rounds of replication. Such defective viruses
can be produced by co-transfecting vaccinia vectors lacking
30 a specific gene(s) required for viral replication into cell
lines which permanently express this gene(s). Viruses
50

5 lacking an essential gene(s) will be replicated in these
cell lines but when administered to the human host will not
be able to complete a round of replication. Such
10 preparations may transcribe and translate — in this
abortive cycle — a sufficient number of genes to induce an
5 immune response.

Alternatively, larger quantities of the strains
can be administered, so that these preparations serve as
15 inactivated (killed) virus, vaccines. For inactivated
vaccines, it is preferred that the heterologous gene
product be expressed as a viral component, so that the gene
20 product is associated with the virion. The advantage of
such preparations is that they contain native proteins and
do not undergo inactivation by treatment with formalin or
other agents used in the manufacturing of killed virus
vaccines.

25 In another embodiment of the invention,
15 inactivated vaccine formulations are prepared using
conventional techniques to "kill" the recombinant viruses.
Inactivated vaccines are "dead" in the sense that their
30 infectivity has been destroyed. Ideally, the infectivity
of the virus is destroyed without affecting immunogenicity.
In order to prepare inactivated vaccines, the recombinant
20 virus may be grown in cell culture or in the allantois of
the chick embryo, purified by zonal ultracentrifugation,
35 inactivated by formaldehyde or β -propiolactone, and pooled.
The resulting vaccine is usually inoculated
intramuscularly.

40 Inactivated viruses may be formulated with a
25 suitable adjuvant in order to enhance the immunological
response. Such adjuvants may include but are not limited
to mineral gels, e.g., aluminum hydroxide; surface active
45 substances such as lysolecithin, pluronic polyols,
polyanions; peptides; oil emulsions; and potentially useful
human adjuvants such as BCG and Corynebacterium parvum.

30

5.2.3. METHODS OF TREATMENT AND/OR VACCINATION

Since the identified target epitopes of the present invention can be produced in large amounts, the antigen thus produced and purified has use in vaccine preparations. The target epitope may be formulated into a subunit vaccine preparation, or may be engineered into viral vectors and formulated into vaccine preparations. Alternatively, the DNA encoding the target epitope may be administered directly as a vaccine formulation. The "naked" plasmid DNA once administered to a subject invades cells, is expressed on the surface of the invaded cell and elicits a cellular immune response, so that T lymphocytes will attack cells displaying the selected epitope. The selected epitope also has utility in diagnostics, e.g., to detect or measure in a sample of body fluid from a subject the presence of tumors and thus to diagnose cancer and tumors and/or to monitor the cellular immune response of the subject subsequent to vaccination.

The recombinant viruses of the invention can be used to treat tumor-bearing mammals, including humans, to generate an immune response against the tumor cells. The generation of an adequate and appropriate immune response leads to tumor regression *in vivo*. Such "vaccines" can be used either alone or in combination with other therapeutic regimens, including but not limited to chemotherapy, radiation therapy, surgery, bone marrow transplantation, etc. for the treatment of tumors. For example, surgical or radiation techniques could be used to debulk the tumor mass, after which, the vaccine formulations of the invention can be administered to ensure the regression and prevent the progression of remaining tumor masses or micrometastases in the body. Alternatively, administration of the "vaccine" can precede such surgical, radiation or chemotherapeutic treatment.

Alternatively, the recombinant viruses of the invention can be used to immunize or "vaccinate" tumor-free

5 subjects to prevent tumor formation. With the advent of
genetic testing, it is now possible to predict a subject's
predisposition for cancers. Such subjects, therefore, may
10 be immunized using a recombinant vaccinia virus expressing
an appropriate tumor-associated antigen.

5 The immunopotency of the epitope vaccine
formulations antigen can be determined by monitoring the
immune response in test animals following immunization or
15 by use of any immunoassay known in the art. Generation of
a cell-mediated immune response may be taken as an
indication of an immune response. Test animals may include
20 mice, hamsters, dogs, cats, monkeys, rabbits, chimpanzees,
etc., and eventually human subjects.

Suitable preparations of such vaccines include
injectables, either as liquid solutions or suspensions;
25 solid forms suitable for solution in, suspension in, liquid
prior to injection, may also be prepared. The preparation
15 may also be emulsified, or the polypeptides encapsulated in
liposomes. the active immunogenic ingredients are often
mixed with excipients which are pharmaceutically acceptable
30 and compatible with the active ingredient. Suitable
excipients are, for example, water, saline, dextrose,
glycerol, ethanol, or the like and combinations thereof.

20 In addition, if desired, the vaccine preparation may also
include minor amounts of auxiliary substances such as
35 wetting or emulsifying agents, pH buffering agents, and/or
adjuvants which enhance the effectiveness of the vaccine.

Examples of adjuvants which may be effective,
40 include, but are not limited to: aluminum hydroxide, N-
25 acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-
acetyl-nor-muramyl-L-alanyl-D-isoglutamine, N-
acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-
45 dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine,
GM-CSF, QS-21 (investigational drug, Progenics
Pharmaceuticals, Inc.), DETOX (investigational drug, Ribi
30 Pharmaceuticals), and BCG.

5

The effectiveness of an adjuvant may be determined by measuring the induction of the cellular immune response directed against the target epitope.

10

The vaccines of the invention may be multivalent or univalent. Multivalent vaccines are made from 5 recombinant viruses that direct the expression of more than one antigen.

15

The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, 10 sustained release formulation, or powder. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc.

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Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for 15 example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is administered by injection, an ampoule of sterile diluent can be provided so that the ingredients may be mixed prior to administration.

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20 In a specific embodiment, a lyophilized epitope of the invention is provided in a first container; a second container comprises diluent consisting of an aqueous solution of 50% glycerin, 0.25% phenol, and an antiseptic (e.g., 0.005% brilliant green).

40

Use of purified antigens as vaccine preparations 25 can be carried out by standard methods. For example, the purified protein(s) should be adjusted to an appropriate concentration, formulated with any suitable vaccine adjuvant and packaged for use. Suitable adjuvants may include, but are not limited to: mineral gels, e.g., 45 aluminum hydroxide; surface active substances such as 30 lysolecithin, pluronic polyols; polyanions; peptides; oil

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55

5 emulsions; alum, and MDP. The immunogen may also be
incorporated into liposomes, or conjugated to
10 polysaccharides and/or other polymers for use in a vaccine
formulation. In instances where the recombinant antigen is
a hapten, i.e., a molecule that is antigenic in that it can
5 react selectively with cognate antibodies, but not
immunogenic in that it cannot elicit an immune response,
15 the hapten may be covalently bound to a carrier or
immunogenic molecule; for instance, a large protein such as
serum albumin will confer immunogenicity to the hapten
coupled to it. The hapten-carrier may be formulated for
20 use as a vaccine.

Many methods may be used to introduce the vaccine
formulations described above into a patient. These
include, but are not limited to, oral, intradermal,
25 intramuscular, intraperitoneal, intravenous, subcutaneous,
intranasal, transdermal, epidural, pulmonary, gastric,
15 intestinal, rectal, vaginal, or urethral routes. When the
method of treatment uses a live recombinant vaccinia
vaccine formulation of the invention, it may be preferable
30 to introduce the formulation via the natural route of
infection of the vaccinia virus, i.e., through a mucosal
membrane or surface, such as an oral, nasal, gastric,
20 intestinal, rectal, vaginal or urethral route. To induce a
CTL response, the mucosal route of administration may be
35 through an oral or nasal membrane. Alternatively, an
intramuscular or intraperitoneal route of administration
may be used. Preferably, a dose of 10^6 - 10^7 PFU (plaque
40 forming units) of cold adapted recombinant vaccinia virus
25 is given to a human patient.

The precise dose of vaccine preparation to be
employed in the formulation will also depend on the route
45 of administration, and the nature of the patient, and
should be decided according to the judgment of the
practitioner and each patient's circumstances according to
30 standard clinical techniques. An effective immunizing

5 amount is that amount sufficient to produce an immune response to the antigen in the host to which the vaccine preparation is administered.

10 Where subsequent or booster doses are required, a modified vaccinia virus such as MVA can be selected as the
5 parental virus used to generate the recombinant. Alternatively, another virus, e.g., adenovirus, canary pox virus, or a subunit preparation can be used to boost.
15 Immunization and/or cancer immunotherapy may be accomplished using a combined immunization regimen, e.g., immunization with a recombinant vaccinia viral vaccine of
10 the invention and a boost of a recombinant vaccinia viral vaccine. In such an embodiment, a strong secondary CD8⁺ T cell response is induced after priming and boosting with
20 different viruses expressing the same epitope (for such methods of immunization and boosting, see, e.g., Murata et al., Cellular Immunol. 173:96-107). For example, a patient
25 is first primed with a vaccine formulation of the invention comprising a recombinant vaccinia virus expressing an epitope, e.g., a selected tumor-associated antigen or fragment thereof. The patient is then boosted, e.g., 21
30 days later, with a vaccine formulation comprising a recombinant virus other than vaccinia expressing the same epitope. Such priming followed by boosting induces a
20 strong secondary CD8⁺ T cell response. Such a priming and boosting immunization regimen is preferably used to treat a
35 patient with a tumor, metastasis or neoplastic growth expressing the selected tumor-associated antigen.

40 In yet another embodiment, the recombinant
25 vaccinia viruses can be used as a booster immunization subsequent to a primary immunization with inactivated tumor cells, a subunit vaccine containing the tumor-associated
45 antigen or its epitope, or another recombinant viral vaccine, e.g., adenovirus, canary pox virus, or MVA.

In an alternate embodiment, recombinant vaccinia
30 virus encoding a particular tumor-associated antigen, epitope or fragment thereof may be used in adoptive

5 immunotherapeutic methods for the activation of T
lymphocytes that are histocompatible with the patient and
specific for the tumor-associated antigen (for methods of
10 adoptive immunotherapy, see, e.g., Rosenberg, U.S. Patent
No. 4,690,915, issued September 1, 1987; Zarling, et al.,
5 U.S. Patent No. 5,081,029, issued January 14, 1992). Such
T lymphocytes may be isolated from the patient or a
histocompatible donor. The T lymphocytes are activated in
15 vitro by exposure to the recombinant vaccinia virus of the
invention. Activated T lymphocytes are expanded and
inoculated into the patient in order to transfer T cell
10 immunity directed against the tumor-associated antigen
epitope.

The invention also provides a pharmaceutical pack
or kit comprising one or more containers comprising one or
25 more of the ingredients of the vaccine formulations of the
invention. Associated with such container(s) can be a
15 notice in the form prescribed by a governmental agency
regulating the manufacture, use or sale of pharmaceuticals
or biological products, which notice reflects approval by
30 the agency of manufacture, use or sale for human
administration.

20 The invention will be better understood by
reference to the specific embodiments detailed in the
35 examples which follow.

6. **EXAMPLE: TRIMOLECULAR RECOMBINATION
EMPLOYING MODIFIED VACCINIA VIRUS
40 VECTORS TO MAKE EXPRESSION LIBRARIES**

25 This example describes a tri-molecular
recombination method employing modified vaccinia virus
vectors and related transfer plasmids that generates close
45 to 100% recombinant vaccinia virus and, for the first time,
allows efficient construction of a representative DNA
30 library in vaccinia virus.

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6.1. CONSTRUCTION OF THE VECTORS

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The previously described vaccinia virus transfer plasmid pJ/K, a pUC 13 derived plasmid with a vaccinia virus thymidine kinase gene containing an in-frame Not I site (Merchlinisky, M. et al., Virology 190:522-526), was further modified to incorporate a strong vaccinia virus promoter followed by Not I and Apa I restriction sites. Two different vectors, p7.5/tk and pEL/tk, included, respectively, either the 7.5K vaccinia virus promoter or a strong synthetic early/late (E/L) promoter (Fig. 1). The Apa I site was preceded by a strong translational initiation sequence including the ATG codon. This modification was introduced within the vaccinia virus thymidine kinase (tk) gene so that it was flanked by regulatory and coding sequences of the viral tk gene. The modifications within the tk gene of these two new plasmid vectors were transferred by homologous recombination in the flanking tk sequences into the genome of the Vaccinia Virus WR strain derived vNotI⁻ vector to generate new viral vectors v7.5/tk and vEL/tk. Importantly, following Not I and Apa I restriction endonuclease digestion of these viral vectors, two large viral DNA fragments were isolated each including a separate non-homologous segment of the vaccinia tk gene and together comprising all the genes required for assembly of infectious viral particles. Further details regarding the construction and characterization of these vectors and their alternative use for direct ligation of DNA fragments in vaccinia virus are described in section 14 infra.

45

6.2. GENERATION OF AN INCREASED FREQUENCY OF VACCINIA VIRUS RECOMBINANTS

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Standard methods for generation of recombinants in vaccinia virus exploit homologous recombination between a recombinant vaccinia transfer plasmid and the viral

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5 genome. Table 1 shows the results of a model experiment in
which the frequency of homologous recombination following
transfection of a recombinant transfer plasmid into
10 vaccinia virus infected cells was assayed under standard
conditions. To facilitate functional assays, a minigene
5 encoding the immunodominant 257-264 peptide epitope of
ovalbumin in association with H-2K^b was inserted at the Not
1 site in the transfer plasmid tk gene. As a result of
15 homologous recombination, the disrupted tk gene is
substituted for the wild type viral tk+ gene in any
recombinant virus. This serves as a marker for
20 recombination since tk- human 143B cells infected with tk-
virus are, in contrast to cells infected with wild type tk+
virus, resistant to the toxic effect of BrdU. Recombinant
virus can be scored by the viral pfu on 143B cells cultured
in the presence of 125 mM BrdU.
25 The frequency of recombinants derived in this fashion is of
15 the order of 0.1% (Table 1).

Table 1: Generation of Recombinant Vaccinia Virus by
Standard Homologous Recombination

Virus*	DNA	Titer without BrdU	Titer with BrdU	% Recombinant**
vaccinia ----		4.6×10^7	3.0×10^3	0.006
vaccinia 30ng pE/Lova		3.7×10^7	3.2×10^4	0.086
vaccinia 300ng pE/Lova		2.7×10^7	1.5×10^4	0.056

* vaccinia virus strain vNot1

** % Recombinant = (Titer with BrdU/Titer without
BrdU)x100

This recombination frequency is too low to permit
efficient construction of a cDNA library in a vaccinia
vector. The following two procedures were used to generate
an increased frequency of vaccinia virus recombinants.

(i) One factor limiting the frequency of viral
recombinants generated by homologous recombination
following transfection of a plasmid transfer vector into
vaccinia virus infected cells is that viral infection is
highly efficient whereas plasmid DNA transfection is
relatively inefficient. As a result many infected cells do
not take up recombinant plasmids and are, therefore,
capable of producing only wild type virus. In order to
reduce this dilution of recombinant efficiency, a mixture
of naked viral DNA and recombinant plasmid DNA was
transfected into Fowl Pox Virus (FPV) infected mammalian
cells. As previously described by others (Scheiflinger,
F., et al., 1992, Proc. Natl. Acad. Sci. USA 89:9977-9981),
FPV does not replicate in mammalian cells but provides
necessary helper functions required for packaging mature

vaccinia virus particles in cells transfected with non-infectious naked vaccinia DNA. This modification of the homologous recombination technique alone increased the frequency of viral recombinants approximately 35 fold to 3.5% (Table 2).

Table 2: Generation of Recombinant Vaccinia Virus by Modified Homologous Recombination

Virus	DNA	Titer		
		without BrdU	with BrdU	% Recombinant*
FPV	None	0	0	0
None	vaccinia WR	0	0	0
FPV	vaccinia WR	8.9×10^6	2.0×10^2	0.002
FPV	vaccinia WR + pE/Lova (1:1)	5.3×10^4	1.2×10^5	2.264
FPV	vaccinia WR + pE/Lova (1:10)	8.4×10^7	3.0×10^4	3.571

Table 2: Confluent monolayers of BSC1 cells (5×10^5 cells/well) were infected with moi=1.0 of fowlpox virus strain HP1. Two hours later supernatant was removed, cells were washed 2X with Opti-Mem I media, and transfected using lipofectamine with 600ng vaccinia strain WR genomic DNA either alone, or with 1:1 or 1:10 (vaccinia:plasmid) molar ratios of plasmid pE/Lova. This plasmid contains a fragment of the ovalbumin cDNA, which encodes the SIINFEKL epitope, known to bind with high affinity to the mouse class I MHC molecule K^b. Expression of this minigene is controlled by a strong, synthetic Early/Late vaccinia promoter. This insert is flanked by vaccinia tk DNA. Three days later cells were harvested, and virus extracted by three cycles

of freeze/thaw in dry ice isopropanol/ 37°C water bath.
Crude virus stocks were titered by plaque assay on human
TK- 143B cells with and without BrdU.

$$\% \text{Recombinant} = (\text{Titer with BrdU} / \text{Titer without BrdU}) \times 100$$

(ii) A further significant increase in the frequency of viral recombinants was obtained by transfection of FPV infected cells with a mixture of recombinant plasmids and the two large approximately 80 kilobases and 100 kilobases fragments of vaccinia virus v7.5/tk DNA produced by digestion with Not I and Apa I restriction endonucleases. Because the Not I and Apa I sites have been introduced into the tk gene, each of these large vaccinia DNA arms includes a fragment of the tk gene. Since there is no homology between the two tk gene fragments, the only way the two vaccinia arms can be linked is by bridging through the homologous tk sequences that flank the inserts in the recombinant transfer plasmid. The results in Table 3 show that >99% of infectious vaccinia virus produced in triply transfected cells is recombinant for a DNA insert as determined by BrdU resistance of infected tk- cells.

Table 3: Generation of 100% Recombinant Vaccinia Virus using Tri-Molecular Recombination

Virus	DNA	Titer without BrdU	Titer with BrdU	% Recombinant*
FPV	Uncut	2.5×10^6	6.0×10^3	0.24
	v7.5/tk			
FPV	NotI/ApaI	2.0×10^3	0	0
	v7.5/tk arms			
FPV	NotI/ApaI	6.8×10^3	7.4×10^3	100
	v7.5/tk arms + 1:1 pE/Lova			

Table 3: Genomic DNA from vaccinia strain V7.5/tk (1.2 micrograms) was digested with ApaI and NotI restriction endonucleases. The digested DNA was divided in half. One of the pools was mixed with a 1:1 (vaccinia:plasmid) molar ratio of pE/Lova. This plasmid contains a fragment of the ovalbumin cDNA, which encodes the SIINFEKL epitope, known to bind with high affinity to the mouse class I MHC molecule K^b. Expression of this minigene is controlled by a strong, synthetic Early/Late vaccinia promoter. This insert is flanked by vaccinia tk DNA. DNA was transfected using lipofectamine into confluent monolayers (5 X 10⁵ cells/well) of BSC1 cells, which had been infected 2 hours previously with moi=1.0 FPV. One sample was transfected with 600ng untreated genomic V7.5/tk DNA. Three days later cells were harvested, and the virus was extracted by three cycles of freeze/thaw in dry ice isopropanol/ 37° C water bath. Crude viral stocks were plaqued on TK- 143 B cells with and without BrdU selection.

* %Recombinant = (Titer with BrdU/Titer without BrdU)x 100

6.3. CONSTRUCTION OF A REPRESENTATIVE cDNA LIBRARY IN VACCINIA VIRUS

A cDNA library is constructed in the vaccinia vector to demonstrate representative expression of known cellular mRNA sequences.

Additional modifications have been introduced into the p7.5/tk transfer plasmid and v7.5/tk viral vector to enhance the efficiency of recombinant expression in infected cells. These include introduction of translation initiation sites in three different reading frames and of both translational and transcriptional stop signals as well as additional restriction sites for DNA insertion.

5 First, the HindIII J fragment (vaccinia tk gene) of p7.5/tk was subcloned from this plasmid into the HindIII site of pBS phagemid (Stratagene) creating pBS.Vtk.

10 Second, a portion of the original multiple cloning site of pBS.Vtk was removed by digesting the
5 plasmid with SmaI and PstI, treating with Mung Bean Nuclease, and ligating back to itself, generating pBS.Vtk.MCS-. This treatment removed the unique SmaI,
15 BamHI, SalI, and PstI sites from pBS.Vtk.

Third, the object at this point was to introduce a new multiple cloning site downstream of the 7.5k promoter
20 in pBS.Vtk.MCS-. The new multiple cloning site was generated by PCR using 4 different upstream primers, and a common downstream primer. Together, these 4 PCR products would contain either no ATG start codon, or an ATG start codon in each of the three possible reading frames. In
25 addition, each PCR product contains at its 3 prime end, translation stop codons in all three reading frames, and a vaccinia virus transcription double stop signal. These 4
30 PCR products were ligated separately into the NotI/ ApaI sites of pBS.Vtk.MCS-, generating the 4 vectors, p7.5/ATG0/tk, p7.5/ATG1/tk, p7.5/ATG3/tk, and p7.5/ATG4/tk whose sequence modifications relative to the p7.5/tk vector
35 are shown in Figure 2. Each vector includes unique BamHI, SmaI, PstI, and SalI sites for cloning DNA inserts that employ either their own endogenous translation initiation site (in vector p7.5/ATG0/tk) or make use of a vector translation initiation site in any one of the three
40 possible reading frames (p7.5/ATG1/tk, p7.5/ATG3/tk, and
25 p7.5/ATG4/tk).

In a model experiment cDNA was synthesized from poly-A+ mRNA of a murine tumor cell line (BCA39) and
45 ligated into each of the four modified p7.5/tk transfer plasmids. Twenty micrograms of Not I and Apa I digested v/tk vaccinia virus DNA arms an equal was transfected
50 together with an equimolar mixture of the four recombinant plasmid cDNA libraries into FPV helper virus infected BSC-1

5 cells for tri-molecular recombination. The virus harvested had a total titer of 6×10^6 pfu of which greater than 90% were BrdU resistant.

10 In order to characterize the size distribution of cDNA inserts in the recombinant vaccinia library,
5 individual isolated plaques were picked using a sterile pasteur pipette and transferred to 1.5ml tubes containing 100 μ l Phosphate Buffered Saline (PBS). Virus was released
15 from the cells by three cycles of freeze/thaw in dry ice/isopropanol and in a 37° C water bath. Approximately one third of each virus plaque was used to infect one well
20 of a 12 well plate containing tk- human 143B cells in 250 μ l final volume. At the end of the two hour infection period each well was overlayed with 1 ml DMEM with 2.5% fetal bovine serum (DMEM-2.5) and with BUdR sufficient to bring the final concentration to 125 μ g/ml. Cells were
25 incubated in a CO₂ incubator at 37°C for three days. On the third day the cells were harvested, pelleted by centrifugation, and resuspended in 500 μ l PBS. Virus was released from the cells by three cycles of freeze/ thaw as
30 described above. Twenty percent of each virus stock was used to infect a confluent monolayer of BSC-1 cells in a 50mm tissue culture dish in a final volume of 3 ml DMEM-
20 2.5. At the end of the two hour infection period the cells were overlayed with 3 ml of DMEM-2.5. Cells were incubated in a CO₂ incubator at 37°C for three days. On the third day the cells were harvested, pelleted by centrifugation, and resuspended in 300 μ l PBS. Virus was released from the
40 cells by three cycles of freeze/ thaw as described above.
25 One hundred microliters of crude virus stock was transferred to a 1.5 ml tube, an equal volume of melted 2% low melting point agarose was added, and the virus/agarose
45 mixture was transferred into a pulsed field gel sample block. When the agar worms were solidified they were removed from the sample block and cut into three equal
30 sections. All three sections were transferred to the same 1.5 ml tube, and 250 μ l of 0.5M EDTA, 1% Sarkosyl, 0.5mg/ml

5 Proteinase K was added. The worms were incubated in this
solution at 37°C for 24 hours. The worms were washed
several times in 500µl 0.5X TBE buffer, and one section of
10 each worm was transferred to a well of a 1% low melting
point agarose gel. After the worms were added the wells
5 were sealed by adding additional melted 1% low melting
point agarose. This gel was then electrophoresed in a
Bio-Rad pulsed field gel electrophoresis apparatus at
15 200volts, 8 second pulse times, in 0.5X TBE for 16 hours.
The gel was stained in ethidium bromide, and portions of
agarose containing vaccinia genomic DNA were excised from
20 the gel and transferred to a 1.5 ml tube. Vaccinia DNA was
purified from the agarose using β-Agarase (Gibco) following
the recommendations of the manufacturer. Purified vaccinia
DNA was resuspended in 50 µl ddH₂O. One microliter of each
DNA stock was used as the template for a Polymerase Chain
25 Reaction (PCR) using vaccinia TK specific primers MM428 and
15 MM430 (which flank the site of insertion) and KlenTaq
Polymerase (Clontech) following the recommendations of the
manufacturer in a 20µl final volume. Reaction conditions
30 included an initial denaturation step at 95°C for 5 minutes,
followed by 30 cycles of: 94°C 30 seconds, 55°C 30 seconds,
68°C 3 minutes. Two and a half microliters of each PCR
20 reaction was resolved on a 1% agarose gel, and stained with
ethidium bromide. Amplified fragments of diverse sizes
35 were observed. When corrected for flanking vector
sequences amplified in PCR the inserts range in size
between 300 and 2500 bp.

40 The vaccinia virus cDNA library was further
25 characterized in terms of the representation of clones
homologous to the murine alpha tubulin sequence. Twenty
separate pools with an average of either 300, 900 or 2,700
45 viral pfu from the library were amplified by infecting a
monolayer of 143B tk- cells in the presence of BrdU. DNA
was extracted from each infected culture after three days
30 and assayed for the presence of an alpha tubulin sequence
by PCR with tubulin specific primers. Poisson analysis of
50

5 the frequency of positive pools indicates a frequency of
one alpha tubulin recombinant for every 2000 to 3000 viral
10 pfu. This is not significantly different from the expected
frequency of alpha tubulin sequences in this murine tumor
cell line and suggests representative expression of this
5 randomly selected sequence in the vaccinia cDNA library.

15 6.4. DISCUSSION

The above-described tri-molecular recombination
strategy yields close to 100% viral recombinants. This is
20 a highly significant improvement over current methods for
generating viral recombinants by transfection of a plasmid
transfer vector into vaccinia virus infected cells. This
latter procedure yields viral recombinants at a frequency
of the order of only 0.1%. The high yield of viral
25 recombinants in tri-molecular recombination makes it
possible, for the first time, to efficiently construct
15 genomic or cDNA libraries in a vaccinia virus derived
vector. In the first series of experiments a titer of 6×10^6
recombinant virus was obtained following transfection
with a mix of 20 micrograms of Not I and Apa I digested
30 vaccinia vector arms together with an equimolar
concentration of tumor cell cDNA. This technological
20 advance creates the possibility of new and efficient
screening and selection strategies for isolation of
35 specific genomic and cDNA clones.

The tri-molecular recombination method as herein
disclosed may be used with other viruses such as mammalian
40 viruses including vaccinia and herpes viruses. Typically,
25 two viral arms which have no homology are produced. The
only way that the viral arms can be linked is by bridging
through homologous sequences that flank the insert in a
transfer vector such as a plasmid. When the two viral arms
45 and the transfer vector are present in the same cell the
only infectious virus produced is recombinant for a DNA
30 insert in the transfer vector.

5 Libraries constructed in vaccinia and other
mammalian viruses by the tri-molecular recombination method
of the present invention may have similar advantages to
10 those described here for vaccinia virus and its use in
identifying target antigens in the CTL screening system of
5 the invention. Similar advantages are expected for DNA
libraries constructed in vaccinia or other mammalian
viruses when carrying out more complex assays in eukaryotic
15 cells. Such assays include but are not limited to
screening for DNA encoding receptors and ligands of
eukaryotic cells.

20 7. EXAMPLE: INDUCTION OF CYTOTOXIC T CELLS
SPECIFIC FOR HUMAN TUMORS IN
HLA AND HUMAN CD8 TRANSGENIC MICE

25 In this example, HLA and human CD8 transgenic
mice were tolerized with a non-tumorigenic, immortalized
15 normal human cell line that does not express costimulator
activity for murine T cells and were subsequently immunized
with B7 (costimulator) transfected tumor cells derived by
30 *in vitro* mutagenesis or oncogene transformation from that
same normal cell line. The HLA transgene permits selection
of a high affinity, HLA- restricted T cell repertoire in
20 the mouse thymus. In addition, a human CD8 transgene is
required because murine CD8 does not interact efficiently
35 with human class I MHC. Subsequent to immunization with B7
transfected tumor cells, splenic CD8+ T cells are isolated
and stimulated again *in vitro* in the absence of
40 costimulation with non-tumorigenic, immortalized human
25 cells. Two pathways of tolerance induction for antigens
shared by the tumorigenic and non-tumorigenic cell lines
may be activated through these manipulations. As known to
45 those skilled in the art, antigen exposure in very young
mice favors tolerance induction by mechanisms that may
30 include both clonal deletion and induction of T cell
anergy. Further, restimulation of activated T cells

5 through their antigen-specific receptors in the absence of
costimulator activity induces apoptotic elimination of
those T cells. This immunization regimen enriched for
10 tumor-specific CTL that did not crossreact with the
homologous normal cells.

5 A series of tumor cell lines were used that were
all derived from a single immortalized, non-tumorigenic
cell line. The non-tumorigenic cells were used to induce
15 tolerance to the large number of normal human proteins that
are also expressed in tumor cells. Availability of a panel
of tumors independently derived from the same normal cells
20 by diverse carcinogens or oncogene transformation makes it
possible to filter out antigenic changes that are
carcinogen specific or that may arise by random genetic
drift during *in vitro* propagation of a tumor cell line.

25 Cytotoxic T cells specific for human bladder
tumor cell lines were induced and isolated from (HLA-A2/K^b x
15 human CD8)F₁ hybrid double transgenic mice that had been
tolerized to the normal cell line from which the tumors
derive. Neonatal mice were injected intraperitoneally with
30 5×10^6 non-tumorigenic SV-HUC. Seven weeks later they were
immunized with 5×10^6 B7.1 transfected ppT11.B7 tumor
cells. ppT11 is one of several independent tumor cell
20 lines derived from SV-HUC by *in vitro* carcinogenesis
(Christian, et al., 1987, Cancer Res. 47: 6066-6073; Pratt,
et al., 1992, Cancer Res. 52: 688-695; Bookland, et al.,
1992, Cancer Res. 52: 1606-1614). One week after
40 immunization, spleen was removed and a single cell
suspension prepared. CD8 positive T cell precursors were
25 enriched on anti-Lyt-2 coated MACS (Magnetic cell sorting
beads) as recommended by the manufacturer (Miltenyi
Biotech, Sunnyvale, CA). 1.5×10^6 CD8 enriched T cells
45 were then restimulated *in vitro* with 4×10^5 SV-HUC in 3 ml
of RPMI 1640 + 10% fetal bovine serum. The rationale is
30 that any SV-HUC specific T cells that escape neonatal
tolerance induction and are activated *in vivo* by

5 stimulation with crossreactive determinants of ppT11.B7,
might now be induced to undergo apoptosis by restimulation
in vitro with costimulator activity negative SV-HUC cells.
10 After 24 hours, T cells are again stimulated with ppT11.B7
in the presence of 2000 Units/ml of recombinant murine IL-
5 6. On day 7 the cycle of SV-HUC stimulation followed 24
hours later by restimulation with ppT11.B7 is repeated.
15 This second round of stimulation with ppT11.B7 is carried
out in the presence of 10 nanogram/ml recombinant murine
IL-7 and 50 Units/ml recombinant murine IL-2. CTL activity
is determined 5 days later by standard chromium release
20 10 assay from labeled targets SV-HUC, ppT11.B7 and YAC-1, a
cell line sensitive to non-specific killing by murine NK
cells. The results in Table 4 show that CTL from ppT11.B7
immunized mice that were not previously tolerized to SV-HUC
25 are equally reactive with SV-HUC and ppT11 target cells.
In contrast, following neonatal tolerization with SV-HUC,
15 15 cytolytic T cells at an effector:target ratio of 5:1 are
significantly more reactive with ppT11.B7 tumor cells than
30 with SV-HUC. Note that B7 costimulator activity is not
required at the effector stage as similar results are
obtained with B7 transfected or non-transfected target
cells.
20 20

Table 4: Tumor-specific response in (HLA-A2/K^b x human CD8)F₁ hybrid transgenic mice neonatally tolerized with SV-HUC parental cells and then immunized with B7 costimulator transfected ppT11.B7 human bladder tumor cells.

Target	Tolerogen: Immunogen:	Effector:Target ratio			
		None ppT11.B7	5:1	10:1	SV-HUC ppT11.B7
SV-HUC			29	68	14 19
ppT11.B7			14	70	17 51
YAC-1			6	6	nd 3

nd = not done

The significance of this experimental protocol is that it offers a means of selecting murine, HLA-restricted cytolytic T cells specific for human epithelial tumor cells. As noted previously, it has proved exceedingly difficult to isolate such T cells directly from either patient PBL or tumor infiltrating lymphocytes of tumors other than melanoma and perhaps renal cell carcinoma. In addition, as emphasized in section 5.1.1, this same strategy can be implemented in two stages. Differentially immunogenic molecules of the human tumor can first be identified employing tumor-specific CTL restricted to a variety of different animal MHC. These antigens can, as described in Example 12, subsequently be characterized in human subjects or transgenic mice for the ability to be processed and presented in association with different human HLA types. An advantage of this two stage approach is that

5 numerous different MHC molecules are available in a variety
of inbred strains and these can be employed to capture an
10 equally broad range of tumor-specific immunogenic peptides
in the initial screening.

5 8. EXAMPLE: HIGH-THROUGHPUT STRATEGY
FOR SELECTION OF DNA RECOMBINANTS
15 FROM A LIBRARY THAT ENCODES THE
TARGET EPITOPES OF SPECIFIC
CYTOTOXIC T CELLS

10 In this example, a model system was assayed to
determine the level of enrichment that can be obtained
through a procedure that selects for DNA recombinants that
20 encode the target epitopes of tumor specific cytotoxic T
cells.

25 8.1. METHODS AND RESULTS

15 A specific vaccinia recombinant that encodes a
well characterized ovalbumin peptide (SIINFEKL) (SEQ ID
NO: 1) was diluted with non-recombinant virus so that it
30 constituted either 0.2%, 0.01%, or 0.001% of viral pfu.
This ovalbumin peptide is known to be processed and
presented to specific CTL in association with the murine
35 class I MHC molecule H-2K^b. An adherent monolayer of MC57G
cells that express H-2K^b were infected with this viral mix
at m.o.i.=1 (approximately 5 x 10⁵ cell/well). MC57G cells
do not themselves express ovalbumin peptide, but do express
40 H-2K^b, which allows them to associate with and present
ovalbumin peptide to the T cells.

25 Following 12 hours of infection with the
recombinant vaccinia virus expressing ovalbumin peptide,
ovalbumin peptide-specific CTL, derived by repeated in
45 vitro stimulation of ovalbumin primed splenic T cells with
the immunodominant ovalbumin SIINFEKL peptide, were added
for 30 min.

30

During this time, some of the adherent cells infected with a recombinant particle that leads to expression of the ovalbumin peptide interacted with a specific cytotoxic T cell and underwent a lytic event. Cells that underwent a lytic event were released from the monolayer. After 30 min, the monolayer was gently washed, and the floating cells and the remaining adherent cells were separately harvested.

Virus extracted from each cell population was titred for the frequency of ovalbumin recombinant viral pfu. Virus extracted from floating cells was then used as input to another enrichment cycle with fresh adherent MC57G cells and ovalbumin peptide-specific CTL. It was observed that, following enrichment of VVova to greater than 10% of total virus, further enrichment of the recombinant virus was accelerated if the m.o.i. in succeeding cycles was reduced from 1 to 0.1. The results, presented in Table 5, demonstrate marked enrichment of VVova recombinant virus from an initial concentration of 0.2% to 49% or from 0.01% to 39% in 5 enrichment cycles and from 0.001% to 18% in 6 enrichment cycles. Note that with 5×10^5 adherent MC57G cells per well and m.o.i. = 1, an initial concentration of 0.001% VVova recombinant virus is equivalent, on average, to seeding only 5 recombinant pfu among 5×10^5 wild type vaccinia virus in a single culture well. A very substantial enrichment is achieved even under these conditions.

25

Table 5: Multiple Cycles of Enrichment for Vvova

		% VVova in		
		Floating cells*		
Enrichment	cycle #	Exp. 1	Exp. 2	Exp. 3
moi = 1	0	0.2	0.01	0.001
	1	2.1	0.3	nd

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5		2	4.7	1.1	nd
		3	9.1	4.9	nd
		4	14.3	17.9	1.4
10		5	24.6		3.3
		6			18.6

5

moi=0.1 5 48.8 39.3

15

* % Vvova = (Titer with BrdU / Titer without BrdU) x 100
 nd = not determined

10

8.2. DISCUSSION

20

The above-described selection method for isolating DNA clones that encode target epitopes of specific cytotoxic T cells from a viral library is far more efficient than existing methods for accomplishing this same goal. Prior to the present invention, the most widely employed method requires transfection of numerous small pools of recombinant plasmids into separate target populations in order to assay T cell stimulation by a minor component of some pool. Because this requires screening out many negative plasmid pools, it is a far more labor intensive procedure than the positive selection method described herein. For a given investment of resources, the method described here can detect positive DNA clones that occur at a much lower frequency than would otherwise be possible. The design principle of this strategy can be directly extended to screening and selection of DNA clones with specific antibodies as well as with CTL.

40

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9. EXAMPLE: IDENTIFICATION OF POTENTIAL TUMOR-SPECIFIC ANTIGENS THAT ARE DIFFERENTIALLY EXPRESSED IN TUMORS

45

Identification of genes that are differentially expressed in human tumors, cancers, or infected cells could facilitate development of broadly effective human vaccines. Most methods for identification of differential gene

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5 expression are variations of either subtractive hybridization or the more recently described differential display technique.

10 Representational difference analysis (RDA) is a subtractive hybridization based method applied to
5 "representations" of total cellular DNA (Lisitsyn, N. and N., M. Wigler. 1993. Cloning the differences between two
15 complex genomes. Science 259: 946-951). The differential display methods of Liang and Pardee (1992, Science 257:967-971) employ an arbitrary 10 nucleotide primer and anchored oligo-dT to PCR amplify an arbitrary
20 subset of fragments from a more complex set of DNA molecules. As described below (Section 9.2), we have modified differential display to enhance the efficiency with which differentially expressed genes can be
25 identified. In this example we illustrate how application of these methods to a related set of tumors independently
15 derived from a single non-tumorigenic, immortalized cell line facilitates identification of tumor-specific gene products.

30 Experiments described by Sahasrabudhe, et al., (1993, J. Immunology 151:6302-6310), focused on a set of murine tumor cell lines, all of which were independently
20 derived from a single cloned, non-tumorigenic BALB/c embryonic fibroblast cell line. These tumors were of
35 particular interest because they are known to share an immunoprotective antigen. The goal of these experiments was to arrive at a molecular definition of that shared
40 tumor antigen. The ready availability of tumor cells, as
25 well as the normal cells from which they were derived, was exploited for efficient analysis of differential gene expression and tumor immunogenicity by the methods
45 described below.

The availability of multiple tumors independently
derived from the same normal cells by diverse carcinogens
30 (or oncogene transformation) also makes it possible to
50 filter out antigenic changes that are carcinogen specific

5 or that may arise as a result of random genetic drift
during *in vitro* propagation of tumor cells. (See Example
10, where a series of human tumor cell lines is described
that satisfy the requirements of this analysis).

5 The relationship between the process of
transformation and expression of shared tumor rejection
antigens was investigated by characterizing the
15 immunological relationships among a series of murine tumors
(BCA 34, BCA 39, BCA 22, and BCB 13) independently derived
from B/C-N7.1C.1, a contact inhibited, non-tumorigenic
clone of a continuous fibroblast cell line derived from a
20 BALB/c fetus (Collins, et al., 1982, Nature 299: 167; Lin,
et al., 1985, JNCI 74: 1025). Although the proximal cause
of tumor transformation may have been a carcinogen induced
mutation, this model afforded the opportunity to determine
25 if the process of transformation is also associated with
expression of a limited number of shared antigens.

15 As reported by Sahasrabudhe, et al. (1993, J.
Immunology 151: 6302-6310), immunological analysis
demonstrates that three of four B/c.N derived tumors confer
30 crossprotective immunity against each other. Concordant
with the *in vivo* cross-protection data, cytolytic T cell
20 clones from mice immunized with one of the immunologically
related tumors specifically lyse all three immunologically
35 related tumors but, importantly, do not react with the
parental B/c.N cells or with the immunologically
independent BCB 13 tumor. The observation of immunological
40 cross-reactivity among a group of tumors independently
25 derived from a cloned non-tumorigenic parental cell line
strongly suggests that a non-random transformation
associated process gives rise to recurrent expression of
45 the same tumor antigen(s). Two methods for analyzing
differential gene expression, representational difference
analysis (RDA) and modified differential display, were
50 employed to isolate CDNA that might encode the relevant
tumor antigen(s).

5

9.1. REPRESENTATIONAL DIFFERENCE ANALYSIS (RDA)

10

The PCR SELECT™ variation of RDA is marketed by Clontech (Palo Alto, CA). The following general protocol outlined in the text and in Fig. 3 is a summary of the manufacturer's recommendations. cDNA is synthesized from both a tracer (represented by BcA 39 tumor mRNA) and a driver (represented by parental B/c.N mRNA).

15

"Representations" of both tracer and driver cDNA are created by digestion with RsaI which cuts the four-base recognition sequence GTAC to yield blunt end fragments.

20

Adaptors, which eventually serve as primer sites for PCR, are ligated to the 5' ends of *only* the tracer cDNA fragments (Fig. 3). Two aliquots of tracer representation are separately ligated with two different adapters. A series of two hybridizations are carried out. In the first set of hybridizations, each adapter ligated tracer sample is denatured and hybridized with a ten fold excess of the denatured representation of driver cDNA for 8 hours. Under these conditions re-annealing of all molecules is incomplete and some of both the high and low copy molecules remain single stranded. Since re-annealing rates are faster for more abundant species, this leads to normalization of the distribution through relative enrichment of low copy number single stranded molecules. The two hybridization reactions with each of the different adapter ligated tracer cDNA representations are then combined *without fractionation or further denaturation* but with addition of more freshly denatured driver in a second hybridization reaction that is allowed to proceed further to completion, approximately 20 hours.

35

40

45

50

An aliquot of the products from the second hybridization is used as a template for a high stringency PCR reaction, using the known sequences at the 5' ends of the ligated adapters as primers. The key here is that only tumor tracer sequences that 1) remain single stranded through the first hybridization and 2) hybridize to a

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55

5 complementary tracer sequence ligated to the alternate
adapter in the second hybridization can be exponentially
amplified during PCR. This excludes both tracer and driver
10 species that either remain single stranded or that have
hybridized to excess driver (since they have a
5 complementary primer at only one or neither end of the
molecule), as well as tracer sequences that hybridize to a
molecule with the same adapter (because the adapters are
15 longer than the primers and hybridize to their own
complement with higher affinity when it is present on the
opposite end of a denatured single stranded molecule - a
20 reaction termed "Suppression PCR" by Clontech). Finally, a
second high stringency PCR is performed using nested
primers built into the adapters so as to further reduce
background and enrich for differentially expressed
25 sequences. The products of the second PCR are
electrophoresed and visualized on an agarose gel.
15 Individual bands are excised and subcloned for further
analysis.

30
9.2. REPRESENTATIONAL DIFFERENCE
ANALYSIS OF GENES THAT ENCODE
POTENTIAL TUMOR IMMUNOGENS

20 This example describes how the PCR SELECT™ cDNA
35 subtraction method (Clontech Laboratories) was successfully
employed to identify a strong candidate for the shared
tumor antigen in a set of immunologically related murine
tumors.

40 As shown in Fig. 4, subtraction of a fragmented
25 representation of normal cell cDNA from a similar
representation of BCA 39 tumor cDNA resulted in
identification of a series of seven clearly distinguishable
45 subtraction products ranging in size from approximately 300
to 2200 base pairs. To confirm that these DNA fragments
30 were indeed differentially expressed, each band was cloned
into Bluescript plasmid (Stratagene) and the DNA inserts of
50

5 at least 5 colonies from each band were analyzed by
Northern blot hybridization to RNA of the five different
cell lines: the parental cells, the three immunologically
10 crossreactive and the one non-crossreactive tumor cell
line. Representative results for clone 3f derived from RDA
5 band 1 are shown in Fig. 5A.

The probe hybridized to at least three
15 transcripts in the BCA 22, 34 and 39 tumor mRNA.
Expression of these transcripts is unique to these three
immunologically crossreactive tumors. Minimal hybridization
is detected with RNA of the parental B/c.N cells or of the
20 non-crossreactive BCB 13 tumor. Similar results were
obtained in four Northern blots with independent RNA
preparations. The integrity and relative loading of RNA
samples was determined by hybridization to a fragment of
25 the mouse G3PDH gene (Fig. 5B).

The sequence of clone 3f was determined and found
15 to be strongly homologous to a portion of the sequence of a
murine intracisternal type A particle (IAP element) (Aota,
et al., 1987, Gene 56: 1-12). IAPs are endogenous
30 retrovirus-like particles that localize to the cisternae of
the endoplasmic reticulum. They are non-infectious because
they do not encode functional packaging proteins; the
20 potential env region of the sequence contains many
conserved stop codons (Kuff and Lueders, 1988, Advances in
35 Cancer Research 51:183-276). Most IAPs do encode a 73 kDa
major gag protein, and a pol polypeptide with some reverse
transcriptase properties (Wilson and Kuff, 1972, Proc.
40 Natl. Acad. Sci. USA 69: 1531-1536). Expression of IAP
25 transcripts has been described in various mouse primary
tumors (including plasmacytomas, papillomas, carcinomas,
mammary tumors, sarcomas, hepatomas) and established mouse
45 tumors and cell lines (including Friend erythroleukemias,
myelomonocytic leukemia, T lymphomas, myelomas). Although
30 expression in normal thymus may be elevated, only very low
levels of expression are detected in most normal mouse

somatic tissues (Kuff and Lueders, 1988, Advances in Cancer Research 51: 183-276).

9.3. CHARACTERIZATION OF DIFFERENTIALLY
EXPRESSED GENE SEQUENCE FROM RDA

Semi-quantitative PCR is a more sensitive test for differential expression than Northern Blot analysis. Clone 3f sequence specific primers were used to amplify full length oligo- dT primed cDNA from both the BCA 39 tumor and the parental cell line. Amplification with mouse tubulin primers was used to normalize the amount of template between the two cell lines. Equal aliquots of each template were amplified through a variable number of PCR cycles. In each case an estimate of the relative template concentration was derived by fitting a line to the portion of the amplification curve in which product increases exponentially with cycle number. The assumption is that in this region yield is a linear function of (initial template concentration)*(aⁿ) where a = average amplification per cycle in that PCR region, usually between 1.5 and 1.8, and n = cycle number. It was determined that expression of the 3f fragment is at least 7 times greater in the BCA39 tumor cDNA relative to the parental B/c.N.

Differential expression in tumor RNA was confirmed for the inserts of 12 additional clones derived from the six other RDA bands. Northern analysis showed the identical hybridization pattern characteristic of IAP transcripts as observed for clone 3f. The sequence of each clone was determined and found to be homologous to other regions of the IAP genome. A map of the relative position of 10 unique RDA clones is shown in Fig. 6. It can be seen that cumulatively these inserts cover most of the IAP genome.

It is particularly striking that expression of these IAP sequences is shared among the three immunologically crossreactive tumors (BCA 39, BCA 34, and

5 BCA 22) but is absent or very low in both the B/c.N
parental cells and the immunologically unrelated BCB 13
tumor. An IAP epitope is, therefore, a strong candidate
10 for this shared tumor antigen. Experiments are in progress
to transfect the different RDA clones into antigen negative
5 B/c.N cells which will then be tested for sensitization to
lysis by tumor-specific CTL. Transcriptional activation of
endogenous retroviral elements including IAP may represent
15 a new class of shared tumor rejection antigens. It has
been reported (de Bergeyck, et al., 1994, Eur. J. Immunol.
24:2203-2212) that the tumor antigen LEC-A on the murine
20 LEC spontaneous leukemia is also encoded by the gag gene of
an IAP element. Recently, a tumor rejection antigen of a
murine colon tumor, CT26, was found to be encoded by
another type of endogenous retrovirus, a type C particle
25 (Huang, et al., 1996, Proc. Natl. Acad. Sci. USA
93:9730-9735). Retroviral-like elements are also present
15 in the human genome: expression of the pol gene has been
detected in human breast (Moyret, et al., 1988, Anticancer
Res. 8:1279-1283) and colorectal carcinomas (Moshier, et
30 al., 1986, Biochem. Biophys. Res. Commun. 139:1071-1077),
and antibody to the gag gene product has been reported in
20 the sera of patients with human seminoma (Sauter, et al.,
1995, J. Virol. 69:414-421) and renal cell carcinoma
35 (Wahlstrom, et al., 1985, Lab. Invest. 53:464-469).

9.4. MODIFIED DIFFERENTIAL DISPLAY OF GENES ENCODING POTENTIAL TUMOR IMMUNOGENS

40
25 In the following example, the differential
display methods of Liang and Pardee (1992, Science
257:967-971) were modified to improve resolution of DNA
45 fragments and reduce the frequency of false positives.

The differential display method as originally
described by Liang and Pardee (1992, Science 257:967-971)
30 employs an arbitrary 10 nucleotide primer and anchored
oligo-dT to PCR amplify an arbitrary subset of fragments
50

5 from a more complex set of DNA molecules. In principle,
differences among the fragments generated from normal and
tumor cell lines should reflect differences in gene
10 expression in the two cell types. In practice, this method
sometimes works well but often gives rise to numerous false
5 positives. That is, bands which appear to be
differentially displayed are, upon further
15 characterization, found not to be differentially expressed.
This is presumably due to variable PCR amplification of
individual species in complex populations and a relatively
high background that can obscure less prominent bands.
20 Since considerable effort is required to establish
differential expression, these endemic false positives are
costly in terms of efficiency and productivity.

A single arbitrary primer may also be used for
differential display, as described by Welch et al. (3,4).
25 Use of single primers does, however, require synthesis of a
15 much larger set of independent primers to achieve the same
coverage of a complex cDNA population.

Hence, there exists a need for improved
30 differential display methods that improve resolution of DNA
fragments and that reduce the frequency of false positives.

In order to improve the resolution of fragments
20 and reduce the frequency of false positives, a second
35 arbitrary primer was substituted for the anchored oligo-dT
employed in PCR amplification. This results in fewer DNA
products in each PCR reaction so that individual DNA
fragments can be more reliably resolved on sequencing gels.
40

25 Because each subset of fragments generated in
this modified differential display protocol is a smaller
representation of total cDNA, more primer pairs are
45 required for adequate sampling. Employing the negative
binomial distribution, it can be predicted that if 12
independent primers are utilized in all 66 possible primer
30 pair combinations there is a greater than 85% probability
50 that for an average size eukaryotic cDNA at least one

primer pair will amplify a representative PCR fragment of size ≥ 70 bp.

Table 6 lists the sequences of the 12 arbitrary decamers from which primer pairs are selected for modified differential display. The specific primers were chosen on the basis of their sequence diversity, 3' hybridization affinity, and minimal pair-wise hybridization.

TABLE 6: ARBITRARY PRIMERS FOR MODIFIED DIFFERENTIAL DISPLAY

10	20	TAC AAC GAG G MR_1	TCG GTC ACA G MR_9
		GTC AGA GCA T MR_2	ATC TGG TAG A MR_10
		GGA CCA AGT C MR_5	CTT ATC CAC G MR_11
		TCA GAC TTC A MR_7	CAT GTC TCA A MR_12
	25	TAC CTA TGG C MR_8	GAT CAA GTC T MR_14
15	15	TGT CAC ATA C MR_15	CTG ATC CAT G Ldd1

A separate cDNA synthesis reaction with 0.1 μ g polyA-RNA and Superscript II Reverse Transcriptase (Gibco/BRL) is carried out with each primer. Five percent of the cDNA product made with each member of a primer pair is mixed together with that primer pair for amplification in 30 PCR cycles using Klen Taq Polymerase Mix (Clontech). The PCR primers are used for cDNA synthesis to avoid the 3' bias imposed by oligo-dT primed cDNA synthesis. The relative orientation of the two primers in cDNA is randomized by carrying out a separate synthesis with each primer. These cDNA can be mixed in the same combinations as the primers chosen for PCR amplification. PCR amplified cDNA fragments are resolved on 6% acrylamide gels and dried for autoradiography. Those bands which are differentially displayed in at least 2 tumor samples and not in the parental cells are cut out and rehydrated. An aliquot (1/5) of the DNA recovered is reamplified using the same

5 primer set and the same PCR conditions but without addition
of isotope. This second PCR product is resolved on 1%
10 agarose and individual bands are recovered by incubation
with β agarase I (Gibco/BRL). Each DNA fragment recovered
is cloned by blunt end ligation into the pcDNA3.1/Zeo (+)
5 phagemid vector (Invitrogen). Since it is possible that a
single band may include more than one molecular species, at
least 4 different transformants with an insert of
15 appropriate size are picked for further characterization.
Northern analysis, RNase protection assays and
semi-quantitative PCR are employed to confirm differential
20 expression.

20 In murine tumor cell lines, it was observed that
many more differentially expressed gene fragments appear to
be identified by differential display than by RDA. In
25 addition, RDA fragments give positive results on Northern
blots exposed for only a few hours. In contrast, fragments
15 identified by differential display often do not give a
signal on Northern blots even after several days.
Differential expression was, in this case, confirmed by
30 RNase protection and semi-quantitative PCR with sequence
specific primers. These observations are consistent with
the theoretical expectation that, because of the difficulty
20 of driving hybridization of low abundance cDNA to
completion, such sequences will be more readily identified
35 by PCR based differential display than by hybridization
based RDA. There may, in addition, be another reason for
the greater sensitivity of modified differential display.
40 It has been reported (Meyuhas and Perry, 1979, Cell 16:
25 139-148) that mRNA species of low abundance are on average
twice the size of smaller, more stable and more abundant
mRNA species. It is, therefore, more likely that both
45 members of a pair of arbitrary primers will hybridize to
and detect differentially expressed cDNA from the longer
(average 4.9 kb) very diverse 80% of mRNA species that are
30 represented by very few copies per cell than from the

5 shorter (average 2 kb) 20% of mRNA species that are more abundantly expressed.

10 In preliminary experiments, an average of three differentially displayed bands were identified for each pair of primers. With a total of 66 primer pairs generated
5 from all possible combinations of 12 independent primers, approximately 200 gene fragments could be identified. In
15 some cases multiple fragments may derive from the same gene. Fig. 7 shows the pattern of differential display fragments observed with one pair of arbitrary decamers, MR_1 (TAC AAC GAG G) and MR_5 (GGA CCA AGT C). A number of
20 bands can be identified that are associated with all four tumors but not with the parental cells. This distribution is unrelated to the immunogenicity of the tumor cells, since only three of the four tumors are immunologically crossreactive. In contrast to the differentially expressed
25 bands identified by RDA, which gave positive results on Northern blots exposed for only a few hours, fragments identified by differential display did not give a signal on Northern blots even after several days. Differential
30 expression of the differential display fragments can, however, be confirmed by RNase protection assays or by semi-quantitative PCR with sequence specific primers. An
20 example is shown in Fig. 8, the results of an RNase protection assay with clone 90 from differential display band 9. This sequence, which has no significant homology to entries in the GenBank database, is expressed in all
35 four tumor lines but not in the parental B/c.N.

40 As discussed above, we attribute this striking difference in the results of RDA and differential display
25 to the greater sensitivity of the PCR based modified differential display as compared to the hybridization based RDA method. Based on the pattern of expression in the
45 different tumor and normal cell lines, it appears that the shared tumor antigen detected following direct immunization of mice with syngeneic tumor cells may be encoded by a more
30 abundantly expressed IAP gene. The methods described in

5 this example can be used to determine whether the products
of the less abundantly expressed genes identified by
modified differential display represent potential cryptic
10 tumor antigens.

5 9.5. SELECTION OF FULL LENGTH cDNA
ENCODING POTENTIAL TUMOR IMMUNOGENS

15 This section presents methods for facilitating
selection of corresponding full length cDNAs from fragments
of differentially expressed genes identified by
representational difference analysis or by modified
20 differential display (Fig. 9). A single stranded
biotinylated probe is synthesized from isolated cDNA
fragments and is used to select the longer cDNA that
contain a complementary sequence by solution hybridization
to single stranded circles rescued from a phagemid tumor
25 cDNA library. This method is especially well-suited to the
15 use of DNA fragments isolated by the modified differential
display method employing two arbitrary primers. The same
arbitrary primers employed for PCR amplification of a given
30 fragment in differential display can be modified to
generate a single stranded hybridization probe from that
fragment. This avoids the need to sequence, select and
20 synthesize a new pair of fragment specific primers for each
35 new fragment of interest.

i) The two oligonucleotides of a pair of PCR primers
employed in differential display are modified:
40 (biotin-dT)-dT- (biotin-dT) is incorporated at the 5' end
of one primer and a phosphate is incorporated at the 5' end
25 of the second primer. These modified primers are
incorporated by PCR into the two strands of a differential
display fragment that was selected following the original
45 PCR amplification with the same unmodified arbitrary
primers. From this double stranded PCR product, the strand
30 labelled with a 5' phosphate is digested with λ exonuclease
to generate a single stranded biotin-labeled probe.

5 ii) Single stranded (ss) DNA circles are rescued from
a phagemid cDNA library using the M13K07 packaging
defective phage as helper virus. This library is
constructed in the pcDNA3.1/Zeo(+) phagemid (Invitrogen,
10 Carlsbad, CA) with insertion of (ApaI)oligo-dT primed cDNA
5 between the Apa I and Eco RV restriction sites. A key
manipulation to achieve the efficient ligation necessary
for construction of a high titer cDNA library is to insure
15 that cDNA inserts are 5' phosphorylated by treating with T4
polynucleotide kinase prior to ligation. The
biotin-labeled single stranded probe generated from the
20 differential display fragment is hybridized in solution to
the ssDNA circles of the phagemid library. The
biotin-labeled hybridization complexes can then be
separated from unrelated ssDNA on streptavidin magnetic
beads and the ss circles eluted for further analysis (Fig.
25 9).

15 As a test of this enrichment method, a model
plasmid mix was prepared that included 1% of a specific
arbitrarily selected recombinant clone, 3f IAP. A
30 biotinylated ss-probe was prepared from the 3f RDA fragment
and used to select single stranded phagemid circles from
the 1% plasmid mix. Following elution from streptavidin
20 beads, the single stranded circles were hybridized to a
sequence specific oligonucleotide in order to prime
35 synthesis of the second plasmid strand prior to bacterial
transformation. Plasmid DNA was prepared from 63
transformed colonies. 63 of 63 of these plasmid
40 preparations expressed the target 3F IAP insert. This
25 method therefore appears to be very efficient.

The same method appears to work with similar
efficiency in the more stringent case of a differential
45 display fragment (B4) representing a previously
unidentified sequence that is expressed in all four murine
tumors at a concentration approximately 10 fold greater
30 than in the non-tumorigenic parental cells. 5 out of 5
50 transformants randomly picked following selection of single

strand circles with the 200 bp B4 DNA fragment had longer inserts that were positive by PCR with sequence specific primers. This method therefore appears to be very efficient.

10. EXAMPLE: INDEPENDENT HUMAN TUMOR CELL
LINES DERIVED FROM A NON-TUMORIGENIC,
IMMORTALIZED CELL LINE

The following example describes a set of human tumors independently derived by different carcinogens or oncogene transformation from the same cloned, non-tumorigenic parental cell line. As in the previous examples of the use of RDA and modified differential display for identification of gene products differentially expressed in murine tumors, the availability of related normal and tumor cell lines has considerable advantages for the molecular and immunological analysis of potential cancer vaccines. This not only provides a readily available source of normal control cells and RNA, but also makes it possible to focus on molecular features that are carcinogen independent and, since they are shared by multiple independent tumors, are unlikely to be the products of random genetic drift during in vitro propagation.

A set of human uroepithelial tumors have been derived in the laboratory of Dr. Catherine Reznikoff (University of Wisconsin, Madison) from an SV40 immortalized human uroepithelial cell line, SV-HUC, that is itself contact inhibited, anchorage dependent and non-tumorigenic in nude mice (Christian, et al., 1987, Cancer Res. 47: 6066-6073). A series of independent tumor cell lines were derived by either ras transformation (Pratt, et al., 1992, Cancer Res. 52: 688-695) or in vitro mutagenesis of SV-HUC with different carcinogens including some that are bladder-specific (Bookland, et al., 1992, Cancer Res. 52: 1606-1614). Transformed cells were

initially selected on the basis of altered *in vitro* growth requirements and each was shown to be tumorigenic in nude mice. A subset of these tumors is selected that retain the phenotype of transitional cell carcinoma. Table 7 lists the parental cells and the carcinogens employed to derive these 5 tumor lines *in vitro*. A systematic program is undertaken to 1) identify full length cDNA differentially expressed in these tumors and 2) to test the immunogenicity in HLA and human CD8 transgenic mice of these cDNA products cloned into a vaccinia virus expression vector.

10

TABLE 7: HUMAN UROEPITHELIAL CELL LINES

Acquired from Dr. Catherine A. Reznikoff, University of Wisconsin Clinical Cancer Center

Parental Line	Immortalization
SV-HUC	SV40 immortalized normal bladder epithelial cells
Tumor Line	Carcinogen or Oncogene transformation
MC pT7	3-methylcholanthrene
20 MC ppT11-A3	3-methylcholanthrene followed by 4-aminobiphenyl
MC ppT11-HA2	3-methylcholanthrene followed by N-hydroxy-4-acetylaminobiphenyl
HA-T2	N-hydroxy-4-aminobiphenyl
40 SV-HUC/ <i>ras</i> -T	EJ/ <i>ras</i>

25

Experiments apply both representational difference analysis and modified differential display to identify gene fragments differentially expressed in the MC ppT11-A3 tumor (ppT11A3) relative to the parental SV-HUC. All differentially expressed fragments are tested by Northern analysis and RNase protection assay for parallel

5 expression in mRNA of the other tumor cell lines. Only
those DNA clones expressed in at least 3 of the 5 SV-HUC
derived tumor cell lines are selected for further
10 characterization.

Similar analysis of tumor-specific gene products
5 can be carried out with tumors derived from SV40 large T or
HPV E6 or E7 immortalized cell lines representative of
other human tissues. Published examples include: prostatic
15 epithelium (Parda et al., 1993, The Prostate 23: 91-98,),
mammary epithelium (Band et al., 1990, Cancer Res. 50:
7351-73-57), and bronchial epithelium (Gerwin et al., 1992,
20 Proc. Natl. Acad. Sci. USA 89: 2759-2763; Klein-Szanto et
al., 1992, Proc. Natl. Acad. Sci. USA 89: 6693-6697).

11. EXAMPLE: GENE EXPRESSION IN FRESH
PATIENT BLADDER TUMORS

25 The above-described methods for identification of
15 differentially expressed genes require that both tumor and
normal control cell mRNA be readily available. The
preceding section focuses on tumors derived *in vitro* from
30 immortalized cell lines, from which mRNA may be readily
obtained in large quantities.

20 In spite of the advantages of working with *in*
35 *vitro*-derived tumors from which mRNA may be readily
obtained, it is necessary to address the possibility that
some transformation-associated gene expression might be
missed or, conversely, that some differential gene
40 expression detected might not be transformation related.
25 Although the normal control is contact inhibited, anchorage
dependent and non-tumorigenic, it is likely that it has
undergone some pre-neoplastic event that is the basis for
45 continuous growth *in vitro*. Perhaps a greater concern is
that extraneous gene expression associated with *in vitro*
proliferation might be identified. Two strategies to
30 exclude such events are employed. First, genes are

5 analyzed that are expressed in at least 3 of the 5 bladder
tumor lines but that are not expressed in the *in vitro*
adapted parental cells. This will a) filter out any
10 systematic gene expression selected by *in vitro* growth,
5 since this should be shared by the normal parental cells;
and b) identify any alterations in gene expression that
are carcinogen specific or that may arise as a result of
15 random genetic drift during *in vitro* propagation, since it
is not expected that these would be shared by multiple
independent tumors derived by diverse carcinogens (or
20 oncogene transformation). Second, and most important, only
those differentially expressed genes that can also be shown
to be expressed in multiple samples of fresh patient tumor
material are selected for further characterization.

Patient tumor material together with normal
25 bladder epithelium is cryopreserved following surgery. In
15 comparison to some other carcinomas, normal tissue control
is readily available from bladder cancer patients. Total
RNA is extracted from frozen samples by the acid
30 guanidinium isothiocyanate method (Lee and Costlow, 1987,
Methods in Enzymology 152:633-648). Following Dnase I
treatment, polyA mRNA is fractionated on oligo dT beads and
20 gene expression is analyzed by Northern blot, RNase
protection assay, and semi-quantitative RT/PCR. For each
35 differentially expressed gene fragment identified in the *in*
vitro tumor lines, expression of the gene is characterized
in a panel of 20 patient tumors and normal tissue controls.
40 This sample size permits the estimation of the proportion
25 of patients expressing the gene with a standard error no
greater than 0.11% ($SE = \sqrt{p \cdot (1-p) / n}$ where $p = \text{true}$
proportion and $n = \text{sample size}$. SE is maximal for $p = 0.5$, at
45 that proportion, 10/20 patients, $SE = \pm 0.11$; for any other
value of p , SE is smaller.) Expression of some of these
genes may be correlated in the different tumor samples.
30 This is useful because it creates the possibility of

5 multiple T cell epitopes that could associate with
different human MHC molecules.

10 The expression pattern is also determined, in
other normal adult and fetal tissues, of any gene that is
differentially expressed in bladder tumors relative to
5 normal bladder epithelium. Total RNA or first strand cDNA
prepared from over 30 different human normal adult or fetal
tissues (Discovery Line™ RNA and Gene Pool™ cDNA,
15 Invitrogen, Carlsbad, CA) is used. Expression in fetal but
not normal adult tissue is particularly interesting and
does not preclude consideration as an immunotherapeutic
20 reagent. Expression of intermediate abundance species are
determined by Northern analysis. Low abundance species are
quantitated by RNase protection assay and semi-quantitative
PCR. Those sequences that are recurrently expressed in
tumors derived from multiple patients and which have the
25 lowest relative expression in normal tissue are selected
15 for further characterization as potential tumor-specific
antigens.

30 12. EXAMPLE: THE USE OF DIFFERENTIALLY
EXPRESSED GENE PRODUCTS TO GENERATE

CTLs

20 CROSSREACTIVE WITH AUTHENTIC TUMORS

35 To identify differentially expressed gene
products that might be candidates for tumor immunotherapy,
it is necessary to have a means of delivering the product
for immunization in an environment in which T cell
40 responses to peptides associated with human HLA can be
25 induced. T cells induced by immunogenic products could
then be tested for crossreactivity on HLA compatible tumors
that express the corresponding mRNA. This example
45 describes the use of HLA and human CD8 transgenic mice for
induction of T cell responses to peptides associated with
30 human HLA. If all these conditions are met: 1) the gene
is differentially expressed in multiple human tumors but

5 not normal tissue counterparts; 2) gene products are
immunogenic in association with HLA; and 3) the specific T
cells induced are crossreactive on human tumor cells, then
10 this would constitute key preliminary data preparative to
initiation of clinical vaccine trials.

5 To determine whether the products of
differentially expressed genes are immunogenic, groups of
three (HLA-A2.1 x huCD8)F₁ transgenic mice are immunized
15 intravenously with 5 x 10⁶ pfu of each specific recombinant
vaccinia virus (Bennink and Yewdell, 1990, Current Topics
in Microbiol. and Immunol. 163: 153-178). After at least
20 two weeks, mice are sacrificed and CD8⁺ splenic T cells are
enriched on anti-CD8 coated magnetic beads. CD8⁺ cytolytic
precursors are restimulated in vitro with parental SV-HUC
cells that are transfected with the recombinant
25 differentially expressed gene previously isolated in the
pcDNA3.1/Zeo(+) plasmid expression vector (Section 9.3).
15 Substitution of the plasmid recombinant in place of the
vaccinia vector for restimulation in vitro is necessary to
avoid a large vaccinia vector specific response. After
30 five days in vitro culture, cytolytic activity is
determined by ⁵¹Cr release from SV-HUC target cells
transfected with either the specific recombinant plasmid or
20 a control ovalbumin gene recombinant.

35 This same cytolytic assay can be readily applied
to determine whether the relevant CTL epitope is also
presented by HLA compatible tumor cells that express the
corresponding mRNA. If T cells are induced in (HLA-A2.1 x
40 huCD8)F₁ transgenic mice, HLA compatible targets include
25 tumor cells that either express native HLA-A2.1 or that
have been transfected with HLA-A2.1. The immunogenicity of
differentially expressed gene products is established and
45 it is determined whether there is a crossreaction with
human tumor cells. This finding, together with the
50 demonstration that the same mRNA is expressed in multiple
samples of fresh patient tumors but not normal tissues

5 (Section 11), is required prior to initiation of a clinical vaccine trial.

10 An important consideration for vaccine development is the extensive polymorphism of human class I HLA. As discussed above, an appealing strategy is to
5 target four major HLA subtypes, A2, A3, B7 and B44, that provide broad coverage across ethnic populations. Many
15 peptides bind to multiple members of a single subtype. If several CTL epitopes are identified for each subtype, then this can greatly facilitate formulation of a broadly effective vaccine.

20 13. EXAMPLE: INDUCTION OF PROTECTIVE IMMUNITY

It is desirable, especially in the case of cryptic tumor antigens encoded by low abundance mRNA, to
25 determine whether a T cell response to differentially expressed gene products confers protective tumor immunity. Since a number of differentially expressed genes have been
15 identified in the murine tumor model described above, such experiments are carried out in mice.

30 It has previously been reported for this murine tumor model (Sahasrabudhe, et al., 1993, J. Immunology 151: 6302-6310) that three of four independently derived tumors
20 are immunologically crossreactive. Many of the differentially displayed bands identified in these tumors
35 are, in contrast, present in all four tumors. It is, therefore, unlikely that the genes from which these fragments derive are immunologically dominant in animals
40 inoculated with these tumors.

25 If it is shown that direct immunization with a recombinant differentially expressed gene does, nevertheless, confer protective immunity, then this
45 provides compelling evidence for the efficacy of vaccination with a cryptic tumor antigen.

30 Groups of 5 mice of the BALB/c strain syngeneic to the murine tumors are immunized with each vaccinia virus

5 recombinant for a full length cDNA differentially expressed
in all four murine tumor lines but not the parental B/c.N
cells (Fig. 7). Each group of mice is assayed for
10 induction of protective immunity by challenge with a
tumorigenic inoculum of 1×10^6 BCA 39 tumor cells
5 (Sahasrabudhe, et al., 1993, J. Immunology 151:6302-6310).
To determine whether protective immunity correlates with
15 relative quantitative expression, independent gene products
are tested that represent different levels of differential
expression as determined by semi-quantitative PCR.

20 14. EXAMPLE: CONSTRUCTION AND
CHARACTERIZATION OF VACCINIA
EXPRESSION VECTORS FOR USE IN VACCINES

This example describes the construction and
25 characterization of a new set of direct ligation vectors
designed to be universally applicable for the generation of
15 chimeric vaccinia genomes. The aim was to modify the
genome of vNotI/tk so as to acquire direct ligation vectors
which are more universally useful. First, the insertion
30 site was changed by placing the sites for two unique
restriction enzymes at the beginning of the thymidine
kinase gene. This allows one to fix the orientation of the
20 insert DNA and eliminates the production of contaminating
wild type genomes after religation of viral arms. Second,
35 in order to generate a direct ligation vector which would
express high levels of protein, the thymidine kinase gene
was preceded by a strong constitutive vaccinia virus
40 promoter.

25 These new ligation vectors contain a pair of
unique restriction sites, NotI and ApaI, to eliminate
religation of poxvirus arms and fix the orientation of the
45 insert DNA behind strongly expressing constitutive vaccinia
promoters. The insertion cassette has been placed at the
beginning of the thymidine kinase gene in vaccinia to
30 utilize drug selection in the isolation of recombinants.

14.1. MATERIALS AND METHODS14.1.1. PLASMID CONSTRUCTION

Pairs of oligonucleotides were constructed which, when annealed, contained the 7.5k gene promoter (MM436:GGCCAAAATTGAAAACTAGATCTATTTATTGCACGCGGCCCATGGGCC C (SEQ ID NO.:φφ) and MM437: GGCCGGGCCCCATGGCGCCCGTGCAATAAATAGATCTAGTTTTTCAATTTTT (SEQ ID NO.: φφ)), or the synthetic EL promoter (MM438:GGCCAAAATTGAAATTTTTTTTTTTTTTTTGAATATAAAGCGGCCCA T GGGCCC (SEQ ID NO.:φφ) and MM439: GGCCGGGCCCCATGGCGCCGCTTTATATTCCAAAAAAAAAAAAATTAATTTCAATTTTT (SEQ ID NO.:φφ)) and restriction sites for NotI and ApaI. The double-stranded oligonucleotides were annealed by ramping from 94° C to 20° C over two hours and ligated into the NotI site present in pJNotI/tk, a plasmid containing the HindIII J fragment from vNotI/tk, resulting in plasmids p7.5/tk and pEL/tk.

A Polymerase Chain Reaction (PCR) was performed on pBI221, a plasmid containing the *E.coli gusA* gene encoding for β-glucuronidase (β-glu), using primers MM440 (GGGAAAGGGGCGGCCCATGTTACGTCCTGTAGAAACC) (SEQ ID NO.:φφ) and MM441 (GGGAAAGGGGGCCCTCATTGTTTGCTCCCTGCTG) (SEQ ID NO.:φφ), or MM440 and MM442 (GGGAAAGGGGCGGCCCTCATTGTTTGCTCCCTGCTG) (SEQ ID NO.:φφ), and the resulting fragment was cloned into pCRII (TA cloning kit, Invitrogen). The plasmids were excised with NotI (MM440/MM442 product) and cloned into pJNot/tk digested with NotI yielding pJNot/tk-GUS, or excised with NotI and ApaI (MM440/MM441 product), and inserted into pEL/tk and p7.5/tk previously digested with ApaI and NotI yielding p7.5/tk-GUS and pEL/tk-GUS.

Pairs of oligonucleotides were constructed which, when annealed, contained the 7.5k gene promoter and the nucleotide sequence encoding for a cytotoxic T-cell epitope for ovalbumin (11) (SIINFEKL; SEQ ID NO:φφ) (75ova: GGCCAAAATTGAAAACTAGATCTATTTATTGCACCATGAGTATAATCAACTTTGAAA

5 A ACTGTAGTGA (SEQ ID NO.: $\phi\phi$) and 75ovarv:
 GGCCTCACTACAGTTTTTCAAAGTTGATTAATACTCATGGTGCAATAAATAGATCTAGT
 T TTTCAATTTTT (SEQ ID NO.: $\phi\phi$) or the EL promoter and the
 10 peptide SIINFEKL (SEQ ID NO: $\phi\phi$) (ELova:
 GGCCAAAAATTGAAATTTTATTTTTTTTTTTTGAATATAAACCATGAGTATAATCAAC
 5 T TTGAAAACTGTAGTGA (SEQ ID NO.: $\phi\phi$) and ELovarv:
 GGCCTCACTACAGTTTTTCAAAGTTGATTATACTCATGGTTTATATTCCAAAAA
 15 A ATAAATTTCAATTTTT (SEQ ID NO.: $\phi\phi$). The double-stranded
 oligonucleotides were annealed by ramping from 94° C to 20°
 C over two hours and ligated into the NotI site present in
 pJNotI/tk, a plasmid containing the HindIII J fragment from
 20 vNotI/tk resulting in plasmids p7.5/tk-ova and pEL/tk-ova.

14.1.2. GENERATION OF RECOMBINANT VIRUSES

Cells and viruses were maintained and manipulated
 as described by Earl, et al. (1991, In Ausubel, et al.,
 25 (eds.), Current Protocols in Molecular Biology. Greene
 Publishing Associates/Wiley Interscience, New York).
 15 Recombinant viruses were made using homologous
 recombination by infecting CV-1 cells at a multiplicity of
 30 infection (moi) of 0.05 and two hours later transfecting
 DNA into the infected cells using lipofectamine (Life
 Technologies Incorporated) as suggested by the
 20 manufacturer. After 72 hours the cells were harvested and
 35 isolated plaques were selected by passage in Hutk cells in
 the presence of bromodeoxyuridine (Earl, et al., 1991, In
 Ausubel, et al. (eds.), Current Protocols in Molecular
 40 Biology. Greene Publishing Associates/Wiley Interscience,
 25 New York) or HAT supplemented media (Weir, et al., 1982,
 Proc. Nat. Acad. Sci. USA, 79:1210-1214).

Vaccinia virus was generated from viral DNA by
 45 rescue with fowlpox virus (Scheifflinger, et al., 1992,
 Proc. Natl. Acad. Sci. USA 89:9977-9981). Vaccinia virus
 was isolated from infected HeLa cells by banding and
 30 sedimentation in sucrose (Earl, et al., 1991, In Ausubel,
 50 et al. (eds.), Current Protocols in Molecular Biology.

5 Greene Publishing Associates/Wiley Interscience, New York).
The purified virions were treated with Proteinase K
(Boehringer Mannheim) and gently extracted with buffer
10 saturated phenol, phenol:chloroform (50:50), and chloroform
before precipitation with 2.5 volumes of ethanol in 0.3M
5 sodium acetate and resuspended in TE (10mM TrisHCl, pH8.0.
1mM EDTA (Earl, et al., 1991, *In* Ausubel, et al. (eds.),
15 Current Protocols in Molecular Biology. Greene Publishing
Associates/Wiley Interscience, New York). Confluent wells
of BSC-1 cells from a 12 well dish were infected with
fowlpox virus and after a two hour incubation at 37° C were
20 transfected with 0.6 µg full length vaccinia DNA using
Lipofectamine (Life Technologies Incorporated) as suggested
by the manufacturer. After 24, 48, and 72 hours the cells
were harvested, lysed by three freeze-thaw cycles and
25 screened by plaque assay on BSC-1 cells (Earl, et al.,
1991, *In* Ausubel, et al., (eds.), Current Protocols in
15 Molecular Biology. Greene Publishing Associates/Wiley
Interscience, New York).

30 14.1.3. GENERATION OF RECOMBINANT
VIRUSES BY DIRECT LIGATION

20 The 1.1 kB Eco RI/ Eco RV restriction
35 endonuclease fragment containing ovalbumin from pHbeta -
Ova-neo (Pulaski, et al., 1996, Proc. Natl. Acad. Sci. USA,
93:3669-3674) was inserted into the EcoRI and EcoRV sites
of pBluescript KS+ (Stratagene), generating pBS.ova. The
40 DNA product from a Polymerase Chain Reaction (PCR) on
25 pBS.ova using primers VV0LZ5
(GCAGGTGCGGCCGCGTGGATCCCCCGGGCTGCAGG) (SEQ ID NO.: φφ) and
VVTLZ3 (GTACCGGGCCCCACAAAACAAAATTAGTTAGTTAGGCCCCCCTCGA)
45 (SEQ ID NO.: φφ) was digested with ApaI and NotI (Life
Technologies, Inc.), gel purified from low melting point
agarose (Bio-Rad) using beta Agarase (Life Technologies,
30 Inc.) following the recommendations of the manufacturer,
50 and cloned into pBluescript KS+ that had been digested with

5 NotI and ApaI, generating pBS.VVova. A DNA fragment
encoding ovalbumin was excised from pBS.VVova by digestion
10 of this plasmid with ApaI and NotI and purified after
electrophoresis through a low melting point agarose gel
using beta Agarase. One microgram of purified vEL/tk DNA
5 was digested with ApaI and NotI and centrifuged through a
Centricon 100 concentrator (Amicon) to remove the small
intervening fragment. The vEL/tk DNA arms and the DNA
15 fragment encoding ovalbumin were ligated overnight at room
temperature, at a 4:1 (insert: virus) molar ratio, in 30
microliters with 5 units T4 DNA Ligase. The ligation
20 product was transfected using lipofectamine (Life
Technologies, Inc.) into a well of confluent BSC-1 cells
from a 12 well plate two hours after infection with fowlpox
virus at 1 pfu/cell. Three days later the cells were
25 harvested and isolated plaques were selected by passage in
Hutk- cells in the presence of bromodeoxyuridine (Earl, et
15 al., 1991 *In* Ausubel, et al. (eds.), *Current Protocols in*
Molecular Biology. Greene Publishing Associates/Wiley
Interscience, New York).

14.1.4. ANALYSIS OF VIRAL DNA GENOMES

20 BSC-1 cells were infected at high multiplicity of
infection (moi) by vaccinia WR, vEL/tk, v7.5/tk, or
35 vNotI/tk. After 24 hours the cells were harvested and
resuspended in Cell Suspension Buffer (Bio-Rad Genomic DNA
Plug Kit) at 1×10^7 cells/ml. An equal volume of 2% CleanCut
40 agarose (Bio-Rad) preincubated at 50° C was added and the
cell suspension was formed into 100 μ l plugs. After
25 hardening at 4° C the plugs were treated as previously
described to digest protein (Merchlinisky, et al., 1989. *J.*
Virology 63:1595-1603). The plugs were equilibrated in the
45 appropriate restriction enzyme buffer and 1mM PMSF for 16
hours at room temperature, incubated with restriction
enzyme buffer, 100ng/ml Bovine Serum Albumin and 50 units
30

5 NotI or ApaI for two hours at 37° C (NotI) or room temperature (ApaI) prior to electrophoresis.

10 One well of a 6 well dish of BSC-1 was infected with v7.5/tk or vEL/tk at high multiplicity of infection (moi) and after 48 hours the cells were harvested, pelleted
5 by low speed centrifugation, rinsed with Phosphate-Buffered Saline (PBS), and the DNA was isolated using DNAzol (Gibco). The final DNA product was resuspended in 50
15 microliters of TE (10mM TrisHCl, pH8.0. 1mM EDTA) and 2.5 microliters were digested with HindIII, HindIII and ApaI, or HindIII and NotI, electrophoresed through a 1.0% agarose
20 gel, and transferred to Nytran (Schleicher and Schuell) using a Turboblotter (Schleicher and Schuell). The samples were probed with p7.5/tk (Figure 11a) or pEL/tk (Figure 11b) labeled with ³²P using Random Primer DNA Labeling Kit (Bio-Rad) in QuickHyb (Stratagene) and visualized on Kodak
25 XAR film.

15 One well of a 6 well dish of BSC-1 cells was infected with v7.5/tk, vEL/tk, vNotI/tk, vpNotI, vNotI/lacZ/tk, or wild type vaccinia WR at high
30 multiplicity of infection (moi) and after 48 hours the cells were harvested, pelleted by low speed centrifugation, rinsed with Phosphate-Buffered Saline (PBS), and the DNA
20 was isolated using DNAzol (Gibco). The final DNA product was resuspended in 50 microliters of TE (10mM TrisHCl, pH8.0. 1mM EDTA) and used in a PCR (30 cycles, 1 minute 94°
35 C, 2 minutes 55° C, 3 minutes 72° C, MJ Research PTC-100) with primers MM407 (GGTCCCTATTGTTACAGATGGAAGGGT) (SEQ ID NO.: $\phi\phi$) and MM408 (CCTTCGTTGCCATACGCTCACAG) (SEQ ID NO.:
40 $\phi\phi$). The nucleotide sequence was determined by ³²S sequencing using Sequenase Version 2.0 DNA Sequencing Kit (Amersham), and visualized after electrophoresis through 8%
45 denaturing polyacrylamide gels by exposure to Bio-Max film (Kodak).

30

14.1.5. DETERMINATION OF β -GLUCURONIDASE ACTIVITY

A well of BSC-1 cells from a 12 well plate was infected at an moi of 1 with vNotI/tk-GUS, v7.5/tk-GUS and vEL/tk-GUS, the cells were harvested 20 hours post infection, resuspended in 0.5ml PBS, and disrupted by three cycles of freeze-thawing. The extract was clarified by a short microfuge spin (one minute, 14,000 rpm) and the supernatant was analyzed for β -glu units as described by Miller, 1972, Experiments in Molecular Genetics, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY as adapted for 96-well plates. The A_{405} values were determined on a microplate reader (Dynatech MR3000) and the β -glu activity was determined by comparison to β -glu (Clontech) standards analyzed in the same assay.

14.1.6. ANALYSIS OF CYTOTOXIC T CELL RESPONSE

Confluent monolayers of MC57G cells in wells of a 6 well plate were infected at an moi of 1 with vEL/tk, v7.5/tk-ova, vEL/tk-ova, vEL/tk-ovaFL clone 1, and vEL/tk-ovaFL clone 2 (vEL/tk-ovaFL are virus clones of full length ovalbumin generated by direct ligation). At 16 hours post infection cells were harvested, labeled with 100 microcuries $^{51}\text{Chromium}$ (Dupont) for 1 hour at 37° C, and 10^4 cells were added to wells of a 96 well round bottom plate in quadruplicate. A sample of uninfected MC57G cells incubated with 1 micromolar purified ova 257-264 peptide was also incubated with ^{51}Cr as a positive control and untreated MC57G cells were used as a negative control. T cells specific for ova 257-264 were added to target cells at ratios of 2:1 and 10:1. Cells were incubated at 37° C for 4 hours, supernatants were harvested, and ^{51}Cr release determined. Spontaneous release was derived by incubating target cells with media alone and maximal release was determined by incubating target cells with 5% Triton X 100. Percentage of specific lysis was calculated using the formula: % specific lysis= ((experimental release-

spontaneous release) / (maximal release-spontaneous release)) X 100. In each case the mean of quadruplicate wells was used in the above formula.

14.2. RESULTS

14.2.1. CONSTRUCTION OF DIRECT LIGATION VECTORS

The vaccinia WR genome is approximately 190 kilobases in length and rich in A and T residues. The complete sequence of the vaccinia WR genome was provided by P. Earl of the Bernard Moss laboratory (Laboratory of Viral Diseases, NIAID, NIH, Bethesda, MD). A restriction enzyme search of the complete sequence of the vaccinia WR genome using MacVector (IBI) revealed a lack of restriction sites for ApaI, AscI, BspI20I, FseI, RsrII, SfiI, SrfI and SgfI. The ready availability of highly active and pure preparations of the enzyme as well as the generation of a staggered end upon digestion led us to choose to use ApaI as the second site in conjunction with the NotI site already present in vNot/tk.

Vaccinia virus based expression vectors are most useful when the foreign protein is expressed constitutively. The expression of foreign proteins during the early stage of viral replication is essential for cytotoxic T cell response (Bennick, et al. 1990, Topics Microbiol. Immunol. 163:153-184) and high levels of total protein expression have been observed using promoters active during the late stage of viral replication. We decided to incorporate the promoters corresponding to the constitutively expressed 7.5k gene (Mackett, et al., 1984, J. Virology, 49:857-864) and a constitutively expressed synthetic promoter EL noted for high level expression.

A useful feature of vNotI/tk that must be retained in any new vector is the ability to discriminate for recombinant viral genomes using selection against an active thymidine kinase gene. The introduction of the ApaI site within the coding sequence for the tk gene

5 necessitates an increase in the total number of amino acids
in order to accommodate the restriction enzyme site. A
comparison of the amino acid sequence for thymidine kinase
10 genes from a variety of animal and viral species showed the
region of greatest heterogeneity was at the N terminus of
5 the protein, suggesting that this region of the protein
could tolerate a modest increase in the number of amino
acids.

15 The recombination-independent cloning vectors
were constructed by making plasmid intermediates containing
the modified thymidine kinase (tk) gene and replacing the
10 tk sequence in the vNotI/tk genome by homologous
recombination. Two sets of oligonucleotide pairs were
constructed which, when annealed, contained the promoter
for the 7.5k gene or the synthetic EL sequence and
restriction sites for NotI and ApaI. The modified
25 thymidine kinase genes were constructed by annealing the
double-stranded oligonucleotides and ligating the product
into the NotI site present at the beginning of the
thymidine kinase gene in pJNotI/tk, a plasmid containing
30 the HindIII J fragment from vNotI/tk. The oligonucleotide
pairs annealed to and eliminated the NotI site in pJNotI/tk
generating a new NotI site closely followed by an ApaI site
20 after the promoter and flanking the nucleotides coding for
the initial methionine in the thymidine kinase gene
resulting in plasmids p7.5/tk and pEL/tk (Figure 1). The
acquisition of the ApaI site was verified by restriction
enzyme analysis of plasmid DNA and the nucleotide sequence
40 of the thymidine kinase gene promoter was determined and
25 found to be as depicted in Figure 1.

The recombinant viruses derived from p7.5/tk and
pEL/tk were isolated using a strategy relying on positive
45 drug selection in the presence of HAT (hypoxanthine,
aminopterin, thymidine) (Weir, et al., 1982, Proc. Nat.
Acad. Sci. USA 79:1210-1214). The viruses vpNotI, a virus
30 that contains a copy of pBR322 inserted at the NotI site of
vNotI/tk (Merchinsky, et al., 1992, Virology 190:522-526),

5 and vNotI/lacZ/tk, a virus with a copy of the lacZ gene
interrupting the thymidine kinase in vNotI⁻ (Merchlinisky, et
al., 1992, Virology. 190:522-526) are thymidine kinase
10 negative (tk⁻) viruses that are identical to vNotI/tk except
for the inserted DNA at the beginning of the tk gene. The
5 plasmids p7.5/tk and pEL/tk were recombined with vpNotI and
vNotI/lacZ/tk helper viruses in CV-1 cells and the infected
monolayers were harvested and passaged in the presence of
15 HAT media on Hutk⁻ cells. Individual plaques were passaged
and isolated an additional three rounds on Hutk⁻ cells
before expansion and analysis.

10

20 14.2.2. ANALYSIS OF THE STRUCTURE OF THE VIRAL GENOMES

The growth of v7.5/tk and vEL/tk virus in HAT
supplemented media implies these viruses, in contrast to
vpNot and vNot/lacZ/tk, contain an active thymidine kinase
25 (tk) gene. However, an active tk gene could arise from
15 multiple crossovers which delete the 7.5k or EL promoter
sequences, generating a virus with the normal tk promoter.
The v7.5/tk and vEL/tk genomes should contain a unique site
for both NotI and ApaI within the HindIII J fragment. The
30 genomic structure of the isolated virus stocks was analyzed
by restriction enzyme digestion of DNA in agarose plugs
20 derived from virus infected cells using NotI or ApaI and
35 electrophoresis of the products through 1% agarose (Figure
10). Uncut vaccinia WR (lane 2) migrates at a size of 190
kilobase pairs as compared to multimers of bacteriophage
lambda (lane 1). After digestion with NotI vaccinia WR is
40 cleaved into two fragments approximately 150 and 40
25 kilobase pairs in length (7th lane from left) whereas the
vNot/tk, vEL/tk, and v7.5/tk were cleaved into fragments of
about 110 and 80 kilobase pairs. When the same samples
45 were digested with ApaI, only one fragment the size of the
uncut genome was observed for both vaccinia WR and vNot/tk
while vEL/tk and v7.5/tk gave the same sized fragments
30 observed after digestion with NotI. Therefore, both

50

55

5 v7.5/tk and vEL/tk contain a unique site for both ApaI and
NotI, the sites are at the same locus as the NotI site in
10 vNot/tk, and the sites are in a more central location in
the genome than the HindIII F fragment which contains the
NotI site in vaccinia WR. The background of cellular DNA
5 fragments was more pronounced in the ApaI digestion, which
has a six base pair recognition site, than for the NotI
digest.

15 The genomes for vEL/tk and v7.5/tk were analyzed
by Southern blotting to confirm the location of the ApaI
and NotI sites in the HindIII J fragment as shown in Figure
20 11. The filters were hybridized to ³²P labeled HindIII J
fragment derived from the p7.5/tk or pEL/tk. The genomes
for v7.5/tk and vEL/tk have an ApaI site that does not
appear in vNotI/tk (compare lanes 7 and 8 to lane 5 in each
blot) whereas digestion with NotI and HindIII yield a set
25 of fragments of equivalent size. The 0.5 kilobase
15 HindIII/NotI or HindIII/ApaI fragment from the left hand
side of HindIII J produced from NotI or ApaI digestion has
electrophoresed off the bottom of the agarose gel.

30 The definitive characterization of the promoter
sequence utilized products of Polymerase Chain Reaction
(PCR). A pair of primers flanking the beginning of the tk
20 gene were used to generate a DNA fragment from the viruses
35 vNotI/tk, v7.5/tk, or vEL/tk and their cognate plasmids as
shown in Figure 12. The PCR products for v7.5/tk and
vEL/tk are the same size as those observed for the plasmids
used to generate the viruses (p7.5/tk and pEL/tk) and
40 larger than those seen for vaccinia WR and vNotI/tk. The
25 PCR fragments were cloned into the plasmid pCRII, the
nucleotide sequence was determined and shown to match the
sequence displayed in Figure 1.

14.2.3. QUANTITATION OF PROMOTER ACTIVITY

The v7.5/tk and vEL/tk vectors have been designed to constitutively express elevated levels of insert protein in comparison to vNotI/tk. The level of RNA synthesis was measured by infecting confluent BSC-1 cells in the presence and absence of cytosine arabinoside (AraC) at an moi of 5, harvesting the cells, isolating the RNA using Trizol (Life Technologies) and analyzing the level of thymidine kinase RNA synthesis by primer extension (Weir, et al., 1990, Nucleic Acids Research 16:10267-10282). Incubation with AraC blocks viral DNA replication, allowing one to identify the class of viral promoter.

The early class of viral promoters are active prior to DNA replication and will be unaffected by AraC in the infection. Late promoters are only expressed after the onset of DNA replication and their activity is abrogated in the presence of AraC. Perusal of the products on a denaturing polyacrylamide gel demonstrated that significantly more (estimated to be at least ten fold) tk RNA primer extension products were synthesized in vEL/tk infections as compared to vNot/tk. In cells infected with vNot/tk a single RNA start site insensitive to AraC incubation was observed whereas in vEL/tk infections two distinct start sites, one resistant to AraC and corresponding to the appropriate early start site (Davison, et al., 1989, J. Mol. Biol. 210:749-769), and one species sensitive to AraC and corresponding to the appropriate late start of RNA (Davison, et al. 1989, J. Mol. Biol. 210:771-784) were observed (data not shown). The pattern of RNA species derived from infection with v7.5/tk was similar to that observed for vEL/tk with the absolute levels of RNA expression intermediate to that observed for vEL/tk and vNot/tk.

In order to verify the levels of expression for genes inserted into the viral vectors the *E.coli gusA* gene encoding for β -glucuronidase (β -glu) was cloned into

5 vNotI/tk, v7.5/tk and vEL/tk viral vectors and the relative
promoter strength was measured. The DNA fragment encoding
for the β -glu gene was inserted into plasmids containing
10 each promoter generating pJNot/tk-GUS, p7.5/tk-GUS and
pEL/tk-GUS. The correct orientation of the insert β -glu
5 gene in pJNot/tk was verified by restriction enzyme
analysis. The plasmids were recombined with vNotI/tk and
the recombinant viruses identified by staining with X-glu
15 (Carroll, et al., 1995, BioTechniques 19:352-355), passaged
for three rounds through Hutk⁻ cells, and expanded to
generate the viral stocks vNotI/tk-GUS, v7.5/tk-GUS and
20 vEL/tk-GUS. The structures of the recombinant viruses were
verified by Southern blot analysis.

The level of expression of β -glu by vNotI/tk-GUS,
v7.5/tk-GUS and vEL/tk-GUS was measured from infected
25 confluent monolayers of BSC-1 cells in the presence or
absence of AraC (Figure 13). The level of β -glu expression
15 for the v7.5/tk-GUS and vEL/tk was much higher than that
observed for vNotI/tk-GUS and highest (approximately twenty
fold higher) in the vEL/tk-GUS. Expression of β -glu was
30 observed for all three viruses in the presence of cytosine
arabioside, indicating that each promoter is a member of
the early class of viral promoters. The level of β -glu in
20 vNotI/tk-GUS was unchanged in the presence or absence of
AraC indicating that this promoter is only active early
35 during infection, whereas the β -glu levels in v7.5/tk-GUS
and vEL/tk-GUS were lower in the presence of AraC,
40 indicating these promoters are active both early and late
times during infection.

25

14.2.4. BIOCHEMICAL CHARACTERIZATION OF VIRUS VECTORS

45 The v7.5/tk and vEL/tk vectors were initially
isolated by growth in the presence of HAT supplemented
media and are designed to contain an active tk gene to
allow selection for viruses with inserts via passage in
30 Hutk⁻ cells in the presence of bromodeoxyuridine (Earl, et

50

55

5 al., 1991, In Ausubel, et al. (eds.), Current Protocols in
Molecular Biology. Greene Publishing Associates/Wiley
Interscience, New York). Both vectors were tested by
10 plaque assay in Hutk⁻ cells using drug selection and the
results for vEL/tk are shown in Figure 14. Incubation
5 without drug or with HAT supplement at a concentration
sufficient to interfere with plaque formation for vpNot or
vNot/lacZ/tk, (data not shown), gave an equivalent number
15 of like-sized plaques. Surprisingly, an equal number of
plaques, albeit much smaller in size, were observed for
vEL/tk with incubation in 25mM bromodeoxyuridine, a
20 concentration sufficient to interfere with the ability of
vaccinia WR to plaque on Hutk⁻ cells (data not shown).
Addition of 125mM bromodeoxyuridine was sufficient to
inhibit plaque formation for vEL/tk (figure 14) and v7.5/tk
25 (data not shown). The higher concentration of
bromodeoxyuridine did not interfere with the growth of tk⁻
15 viruses such as vNotI/lacZ/tk (data not shown) or affect
the viability of the Hutk⁻ cell line.

30 14.2.5. CONSTRUCTION OF RECOMBINANT
VIRUS BY DIRECT LIGATION

20 Direct ligation vectors will only be useful for
the generation of complex expression libraries if the
35 production of infectious virus from the naked DNA is facile
and efficient. Previously, helper virus activity was
supplied in cells transfected with DNA ligation products by
coinfection with conditionally lethal temperature sensitive
40 virus (Merchlinisky, et al., 1992, Virology. 190:522-526) or
25 fowlpox (Scheifflinger, et al., 1992, Proc. Natl. Acad. Sci.
USA, 89:9977-9981). Since high levels of replicating wild
type virus interfere with the ability to package viral DNA
45 and vaccinia virus can recombine with the input DNA, only
conditionally defective vaccinia virus can be used as
50 helper (Merchlinisky, et al., 1992, Virology, 190:522-526).
30 Fowlpox should be a superior helper virus as it is used at

37° C, will not revert to a highly replicating strain, and, since it does not recombine with vaccinia DNA or productively infect primate cell lines, can be used at higher moi than vaccinia. In order to determine if fowlpox can serve as an efficient helper virus a series of wells from a 12 well plate containing BSC-1 cells were infected with varying mois of fowlpox and transfected with full length vaccinia WR DNA, the cells were harvested after 24, 48, or 72 hours and the virus titer was determined as shown in Table 8. Transfection of DNA sans fowlpox or fowlpox infection alone resulted in no plaques. The level of rescued vaccinia increased with later harvest and was proportional to the moi of the fowlpox infection.

TABLE 8		
FPV moi	Day harvested	Titer (pfu x 10 ⁻³)
0.2	1	0
	2	0.12
	3	300
0.5	1	0
	2	0.23
	3	500
1.0	1	0
	2	1.1
	3	700

Table 8. Packaging of vaccinia DNA by fowlpox virus.

Vaccinia DNA was transfected into BSC-1 cells infected with fowlpox virus using lipofectamine as described in Section 14.1 (Materials and Methods). The cells were harvested at 1, 2, or 3 days post transfection, lysed by freeze-thaw cycles and assayed for infectious virus by plaque assay on BSC-1 cells.

A 1.1 kilobase pair fragment of the ovalbumin cDNA (Pulaski, et al., 1996, Proc. Natl. Acad. Sci. USA

5 93:3669-3674) was used as a model insert to study the
generation of functional recombinant virus by direct
ligation. The ovalbumin insert was modified as described
10 in the Materials and Methods to include a NotI site at its
5' end, translation stop codons, a vaccinia transcription
5 stop signal and an ApaI site at its 3' end. This insert
was digested with NotI and ApaI and ligated with purified
vEL/tk DNA arms that had been digested with NotI and ApaI.
15 The ligation mix was transfected into fowlpox infected BSC-
1 cells, cells were harvested, and after three days the
cell extract was passaged on Hutk⁻ cells in the presence or
20 absence of 125mM bromodeoxyuridine. The titer obtained
without drug selection was 2.7×10^3 pfu and with drug
selection 2.3×10^3 pfu. Individual plaques were picked
from Hutk⁻ cells in the presence and absence of
25 bromodeoxyuridine and tested for the presence of the
ovalbumin insert by dot blot hybridization with an
15 ovalbumin cDNA probe. All 15 plaques picked in the
presence of bromodeoxyuridine, and all 10 plaques picked in
its absence contained the ovalbumin insert. These viruses
30 were named vEL/tk-ovaFL. Two individual clones were
expanded further and tested for the ability to sensitize
host cells to lysis by ova 257-264 specific cytotoxic T
20 lymphocytes (CTL). The results of this experiment are
shown in Table 9. As controls, vaccinia recombinant for
an ova 257-264 minigene, v7.5/tk-ova and vEL/tk- ova, were
generated by homologous recombination. These ova peptide
35 recombinant viruses were tested in concert with the vEL/tk-
ovaFL clones for the ability to sensitize host cells to
40 lysis by ova specific CTL. As shown in Table 9, infection
25 with either full length or minigene ovalbumin vaccinia
recombinants was as efficient as pulsing with 1 μ M purified
45 OVA 257-264 peptide for sensitization of target cells to
lysis by OVA-specific CTL.

30

TABLE 9

MC57G cells:	Effector:Target Ratio	
	2:1	10:1
	(Percent Specific Lysis)	
Untreated	-1.3	-1.3
ova257-264 peptide, 1 μ M	54	83
vEL/tk	-0.5	0
v7.5/tk-ova Homologous Recombination	50	78
vEL/tk-ova Homologous Recombination	47	71
vEL/tk-ovaFL Direct Ligation Clone 1	48	70
vEL/tk-ovaFL Direct Ligation Clone 2	46	74

Table 9. CML assay on recombinant vaccinia virus infected cells. Virally infected MC57G cells were generated as described in Section 14.1 (Materials and Methods). One sample of MC57G cells was treated with ova257-264 peptide (1 μ M), another sample of cells was left untreated. Cells were incubated with two different ratios of ova specific cytotoxic T lymphocytes for 4 hours at 37° C and percent specific lysis was determined as described in Section 14.1 (Materials and Methods).

14.3. DISCUSSION

Large DNA viruses are particularly useful expression vectors for the study of cellular processes as they can express many different proteins in their native form in a variety of cell lines. In addition, gene products expressed in recombinant vaccinia virus have been shown to be efficiently processed and presented in association with MHC class I for stimulation of cytotoxic T cells. The gene of interest is normally cloned in a plasmid under the control of a promoter flanked by sequences homologous to a non-essential region in the virus and the cassette is introduced into the genome via

5 homologous recombination. A panoply of vectors for
expression, selection and detection have been devised to
accommodate a variety of cloning and expression strategies.
10 However, homologous recombination is an ineffective means
of making a recombinant virus in situations requiring the
5 generation of complex libraries or when the insert DNA is
large. An alternative strategy for the construction of
15 recombinant genomes relying on direct ligation of viral DNA
"arms" to an insert and the subsequent rescue of infectious
virus has been explored for the genomes of poxvirus
(Merchlinisky, et al., 1992, Virology 190:522-526;
20 Pfleiderer, et al., 1995, J. General Virology 76:2957-2962;
Scheifflinger, et al., 1992, Proc. Natl. Acad. Sci. USA
89:9977-9981), herpesvirus (Rixon, et al., 1990, J. General
Virology 71:2931-2939) and baculovirus (Ernst, et al.,
25 1994, Nucleic Acids Research 22:2855-2856).

Poxviruses are ubiquitous vectors for studies in
15 eukaryotic cells as they are easily constructed and
engineered to express foreign proteins at high levels. The
wide host range of the virus allows one to faithfully
30 express proteins in a variety of cell types. Direct
cloning strategies have been devised to extend the scope of
applications for poxvirus viral chimeras in which the
20 recombinant genomes are constructed *in vitro* by direct
ligation of DNA fragments to vaccinia "arms" and
35 transfection of the DNA mixture into cells infected with a
helper virus (Merchlinisky, et al., 1992, Virology 190:522-
526; Scheifflinger, et al., 1992, Proc. Natl. Acad. Sci. USA
40 89:9977-9981). This approach has been used for high level
25 expression of foreign proteins (Pfleiderer, et al., 1995,
J. Gen. Virology 76:2957-2962) and to efficiently clone
fragments as large as 26 kilobases in length (Merchlinisky,
45 et al., 1992, Virology 190:522-526).

Vaccinia virus DNA is not infectious as the virus
cannot utilize cellular transcriptional machinery and
30 relies on its own proteins for the synthesis of viral RNA.

5 Previously, temperature sensitive conditional lethal
(Merchlinisky, et al., 1992, Virology 190:522-526) or non-
homologous poxvirus fowlpox (Scheifflinger, et al., 1992,
10 Proc. Natl. Acad. Sci. USA 89:9977-9981) have been utilized
as helper virus for packaging. An ideal helper virus will
5 efficiently generate infectious virus but not replicate in
the host cell or recombine with the vaccinia DNA products.
Fowlpox virus has the properties of an ideal helper virus
15 as it is used at 37° C, will not revert to a highly
replicating strain, and, since it does not recombine with
vaccinia DNA or productively infect primate cell lines, can
20 be used at relatively high moi.

The utility of the vaccinia based direct ligation
vector vNotI/tk, has been described by Merchlinisky, et al.
(1992, Virology 190:522-526). This genome lacks the NotI
25 site normally present in the HindIII F fragment and
contains a unique NotI site at the beginning of the
15 thymidine kinase gene in frame with the coding sequence.
This allows the insertion of DNA fragments into the NotI
site and the identification of recombinant genomes by drug
30 selection. The vNotI/tk vector can be used to efficiently
clone large DNA fragments but does not fix the orientation
of the DNA insert or lead to high expression of the foreign
20 protein. This example describes the construction and
characterization of a pair of vaccinia DNA vector genomes
v7.5/tk and vEL/tk suitable for direct ligation. The
v7.5/tk and vEL/tk vectors were designed to contain unique
35 restriction sites for NotI and ApaI at the beginning of the
thymidine kinase gene allowing the oriented cloning of DNA
40 and eliminating the intact genomes arising from relegation
25 of vaccinia vector arms.

The vNotI/tk vector will only express foreign
45 proteins at the level of the thymidine kinase gene, a
weakly expressed gene only made early during viral
infection. To induce high levels of protein expression the
30 sequences encoding for the viral 7.5k promoter and a
50 synthetic EL promoter devised by Chakrabarti and Moss were

5 used to replace the endogenous thymidine kinase promoter.
The levels of expression induced by either promoter was
much higher than that observed in vNotI/tk and the
10 promoters were active at all times post infection. These
continuous expression vectors are applicable in cases
5 dependent on early expression, such as T-cell epitope
presentation, as well as for bulk expression of proteins.

15 Use of the thymidine kinase gene as the insertion
site for foreign DNA allows implementation of selection
protocols for distinguishing recombinants from helper or
wild type genomes. The level of tk expression in v7.5/tk
20 and vEL/tk should be much higher than in vaccinia WR or
vNot/tk. However, the ApaI site at the beginning of the tk
gene in v7.5/tk and vEL/tk was formed from vNot/tk by
adding extra nucleotides at the NotI site. The additional
25 nucleotides increase the amino acid sequence at the N
terminus of the wild type tk gene from Met-Asn-Gly to Met-
15 Gly-Pro-Ala-Ala-Asn-Gly in v7.5/tk and vEL/tk.

Modifications in the expression level and N terminal amino
acid sequence of the thymidine kinase gene may increase
30 (more protein) or decrease (different sequence) the
sensitivity of the virus to bromodeoxyuridine. Plaques,
albeit smaller, were observed with v7.5/tk and vEL/tk
20 infection at a concentration of bromodeoxyuridine
sufficient to completely suppress plaque formation for wild
type vaccinia WR. Plaque formation was suppressed at five-
fold higher concentrations of bromodeoxyuridine, a level of
35 drug that does not interfere with the viability of the
cells or impede the ability of tk virus to form plaques.
40 The explanation for the altered sensitivity to
bromodeoxyuridine awaits further characterization of the
protein as the altered thymidine kinase gene may have a
45 different reaction rate for formation of the triphosphate
form of the bromodeoxyuridine or a reduced ability to bind
bromodeoxyuridine.

30 The development of direct ligation vectors has
increased the possible applications for poxvirus expression
50

5 vectors. The v7.5/tk and vEL/tk vectors were designed to
incorporate the advantages of oriented cloning, high levels
of expression of foreign protein, and the selection for
10 recombinant viruses, into direct ligation vectors. They
were shown to express high levels of proteins at all times
5 during infection. The utility of these vectors was
demonstrated by constructing recombinants containing a CTL
epitope for ovalbumin (constructed by homologous
15 recombination with a plasmid) or the ovalbumin coding
sequence (constructed by direct ligation protocol) and
showing how both recombinants were able to elicit a strong
20 CTL response

The application of these vectors to protocols for
construction of complex expression libraries requires
efficient production of recombinants and strong selection
25 to eliminate or minimize wild type and contaminants. The
use of two restriction sites allows one to design cloning
15 strategies for the oriented cloning of DNA fragments such
as products of PCR (Pfleiderer, et al., 1995, J. General
Virology 76:2957-2962) and increases the frequency of the
desired recombinant as wild type genomes can no longer be
30 generated by ligation of vaccinia arms. When v7.5/tk or
vEL/tk DNA previously digested with NotI and ApaI was
20 transfected into cells infected with fowlpox the virus
titer was one hundred fold lower than for intact uncut DNA.
Also, all plaques isolated in the presence and absence of
35 bromodeoxyuridine (15 with bromodeoxyuridine and 10
without) during the isolation of the vEL/tk-ovaFL contained
40 the ovalbumin insert. The efficiency of infectious virus
25 formation is also increased with the use of fowlpox, helper
virus at relatively high moi. Also, transfection of large
DNA fragments varies with the type and preparation of lipid
45 (Miles Carroll, personal communication) and we are
presently assaying different lipid mixtures and cell types
as well as investigating other parameters to find optimum
30 conditions for the direct ligation protocol. The v7.5/tk

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and vEL/tk vectors provide a set of universally applicable direct ligation cloning vectors for poxviruses.

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The present invention is not to be limited in scope by the specific embodiments described which are intended as single illustrations of individual aspects of the invention, and any constructs, viruses or enzymes which are functionally equivalent are within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

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All publications and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

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WHAT IS CLAIMED IS:

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1. A method for identifying a target epitope comprising screening products of an expression library generated from DNA or RNA derived from a cell expressing the target epitope with cytotoxic T cells generated against the cell to identify DNA clones expressing the target epitope.

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2. The method of Claim 1 wherein the target epitope is specific to a cell infected with a virus, fungus or mycobacteria.

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3. The method of Claim 1 wherein the target epitope is specific to an autoimmune disease.

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4. The method of Claim 1 wherein the expression library is constructed in a viral vector infectious for mammalian cells.

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5. The method of Claim 4 wherein the viral vector is constructed by trimolecular recombination.

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6. The method of Claim 4 wherein the viral vector is a vaccinia viral vector.

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7. A method for identifying a tumor specific target epitope comprising screening products of an expression library generated from DNA or RNA derived from a tumor cell expressing the target epitope with cytotoxic T cells generated against the tumor cell to identify DNA clones expressing the target epitope.

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8. The method of Claim 7 wherein the cytotoxic T cells react with tumor cells derived from a non-tumorigenic cell line and do not cross-react with the non-tumorigenic cell line.

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9. The method of Claim 7 wherein the cytotoxic T cells are derived from animals tolerized with a non-tumorigenic cell line and are then immunized with tumor cells derived from the non-tumorigenic cell line.

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10. The method of Claim 9 wherein the cytotoxic T cells are derived from animals tolerized with a non-tumorigenic cell line that does not express costimulator activity and are subsequently stimulated with a tumor cell line expressing costimulator activity.

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11. The method of Claim 7 wherein the genes expressed in tumor cells are used to generate HLA restricted cytotoxic T cells which are evaluated for activity against tumor cells.

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12. The method of Claim 7 wherein the tumor cell is derived from a single immortalized, non-tumorigenic cell line.

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13. The method of Claim 12 wherein the screening is performed on a panel of tumor cell lines each derived independently from a single non-tumorigenic cell.

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14. The method of Claim 7 wherein the expression library is constructed in a viral vector infectious for mammalian cells.

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15. The method of Claim 14 wherein the viral vector is constructed by trimolecular recombination.

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16. The method of Claim 14 wherein the viral vector is a vaccinia viral vector.

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17. A method for identifying a target epitope or antigen comprising:

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(a) providing cytotoxic T cells specific for a gene product differentially expressed by a cell expressing the target epitope, and

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(b) measuring crossreactivity of the cytotoxic T cells for the cell in which target epitopes are identified as the gene product which induces cytotoxic T cells.

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18. The method of Claim 17 wherein the target epitope is specific to a cell infected with a virus, fungus or mycobacteria.

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19. The method of Claim 17 wherein the target epitope is specific to an autoimmune disease.

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20. The method of Claim 17 wherein a modified differential display method is employed that increases resolution of DNA fragments and reduces the frequency of false positives.

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21. The method of Claim 20 further comprising use of the DNA fragments to isolate longer gene products following solution hybridization to single strand circles rescued from a phagemid DNA library.

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22. A method for identifying a tumor specific target epitope or antigen comprising:

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(a) providing cytotoxic T cells specific for a gene product differentially expressed by a tumor cell expressing the target epitope, and

(b) measuring crossreactivity of the cytotoxic T cells for the tumor cell in which target epitopes are identified as the gene product which induces cytotoxic T cells.

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23. The method of Claim 22 wherein the tumor cell is derived from a single immortalized, non-tumorigenic cell line.

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24. The method of Claim 22 wherein the assay is performed on a panel of tumor cell lines each derived independently from a single non-tumorigenic cell.

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25. The method of Claim 22 wherein the generated cytotoxic T cells which react to tumor cells do not react to nontumorigenic T cells.

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26. The method of Claim 22 wherein a modified differential display method is employed that increases resolution of DNA fragments and reduces the frequency of false positives.

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27. The method of Claim 26 further comprising use of the DNA fragments to isolate longer gene products following solution hybridization to single strand circles rescued from a phagemid DNA library.

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28. A viral vector containing a DNA insert flanked by unique sites for restriction enzymes positioned so that religation of the viral vectors arms is prevented and the orientation of the insert DNA is fixed and the DNA insert is operatively associated with a strong regulatory element.

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29. The viral vector of Claim 28 wherein the vector is constructed by trimolecular recombination.

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30. The viral vector of Claim 28 wherein the viral vector is a vaccinia viral vector.

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31. The vector of Claim 28 in which the vector is derived by recombination with plasmid p7.5/tk (SEQ ID NO:) or derivatives thereof.

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32. The vector of Claim 28 in which the vector is derived by recombination with plasmid pEL/tk (SEQ ID NO:) or derivatives thereof.

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33. A viral vector containing a DNA insert flanked by unique sites for restriction enzymes positioned so that religation of the viral vectors arms is prevented and the orientation of the insert DNA is fixed and the DNA insert is operatively associated with a strong regulatory element wherein the DNA insert encodes a target epitope identified by the method of Claim 1.

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34. A viral vector containing a DNA insert flanked by unique sites for restriction enzymes positioned so that religation of the viral vectors arms is prevented and the orientation of the insert DNA is fixed and the DNA insert is operatively associated with a strong regulatory element wherein the DNA insert encodes a target epitope identified by the method of Claim 7.

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35. The viral vector of Claim 33 or 34 wherein the viral vector is a vaccinia viral vector.

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36. A vaccinia viral vector containing a DNA insert flanked by unique sites for restriction enzymes positioned so that religation of the viral vectors arms is prevented and the orientation of the insert DNA is fixed and the DNA insert is operatively associated with a strong regulatory element wherein the DNA insert encodes a target epitope identified by the method of Claim 17.

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37. A vaccinia viral vector containing a DNA insert flanked by unique sites for restriction enzymes positioned so that religation of the viral vectors arms is prevented and the orientation of the insert DNA is fixed and the DNA insert is operatively associated with a strong regulatory element wherein the DNA insert encodes a target epitope identified by the method of Claim 22.

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38. The viral vector of Claim 36 or 37 wherein the viral vector is a vaccinia viral vector.

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39. A transgenic animal tolerized with a non-tumorigenic cell line that does not express costimulator activity.

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5 40. A transgenic animal according to claim 39, wherein said transgenic animal is further stimulated with a tumor cell line expressing costimulator activity.

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10 41. A cytotoxic T cell derived from the transgenic animal of claim 39.

20 42. A cytotoxic T cell derived from the transgenic animal of claim 40.

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SUBSTITUTE SHEET (RULE 26)

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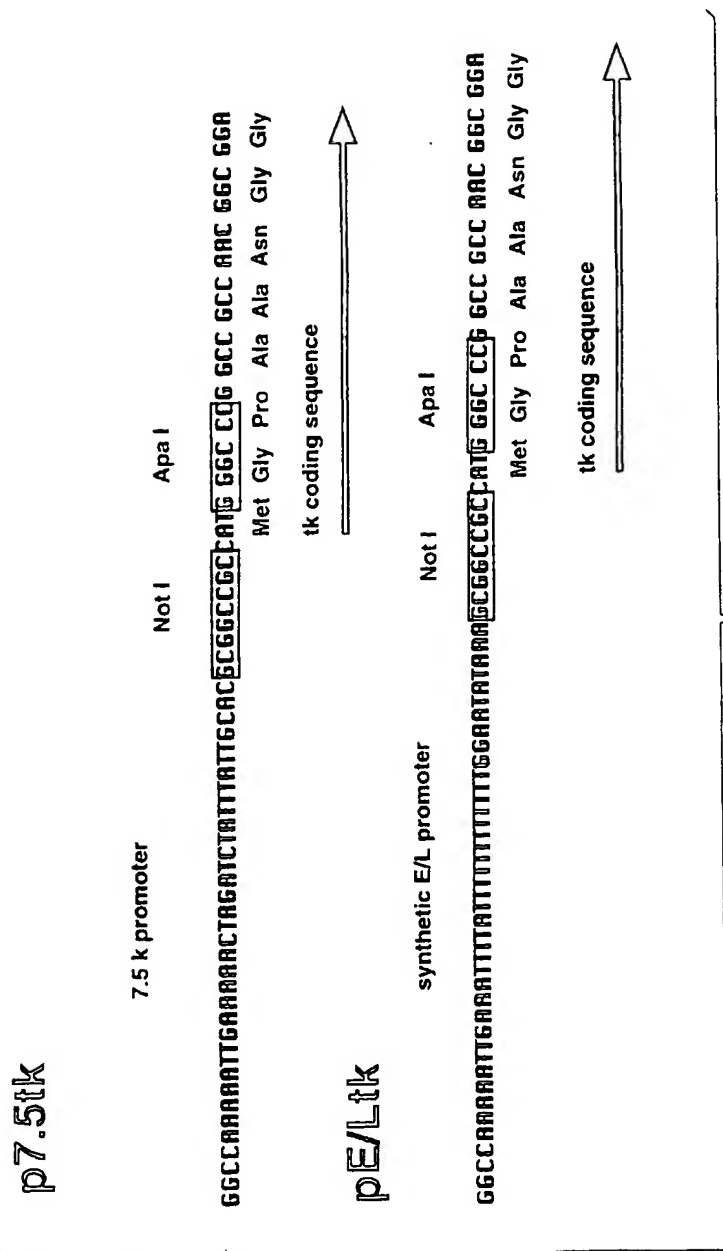


FIG. 1

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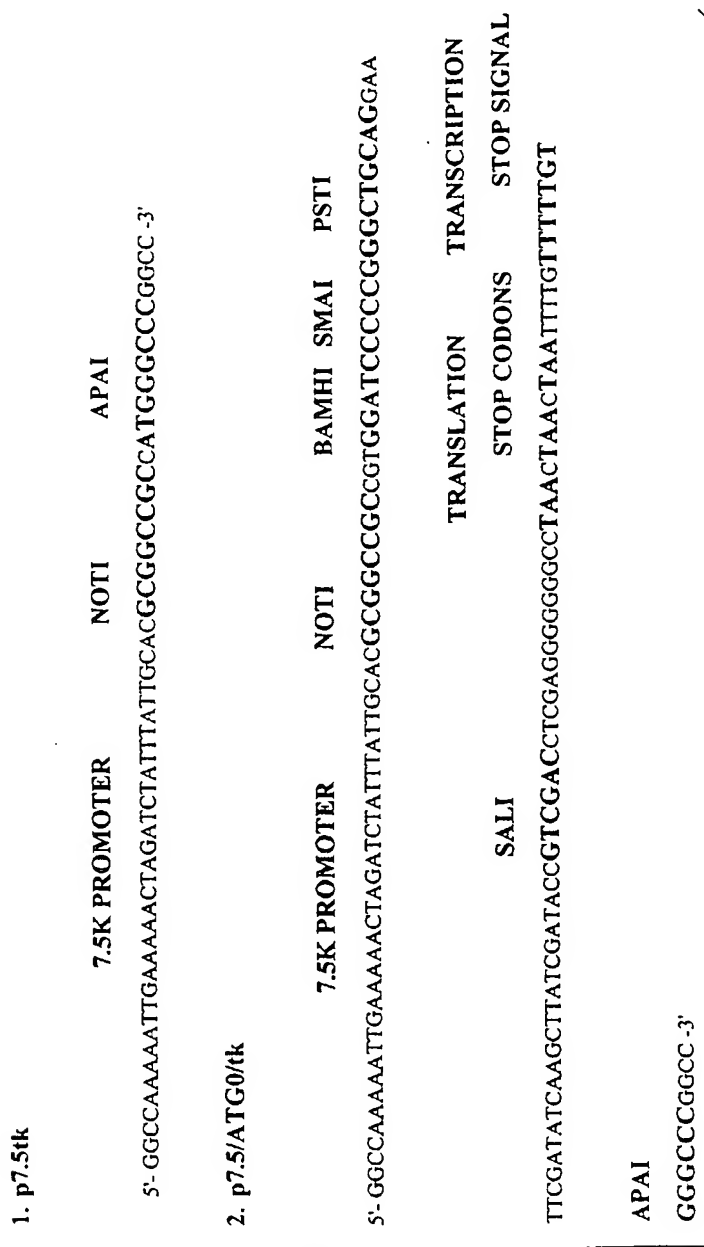


FIG. 2

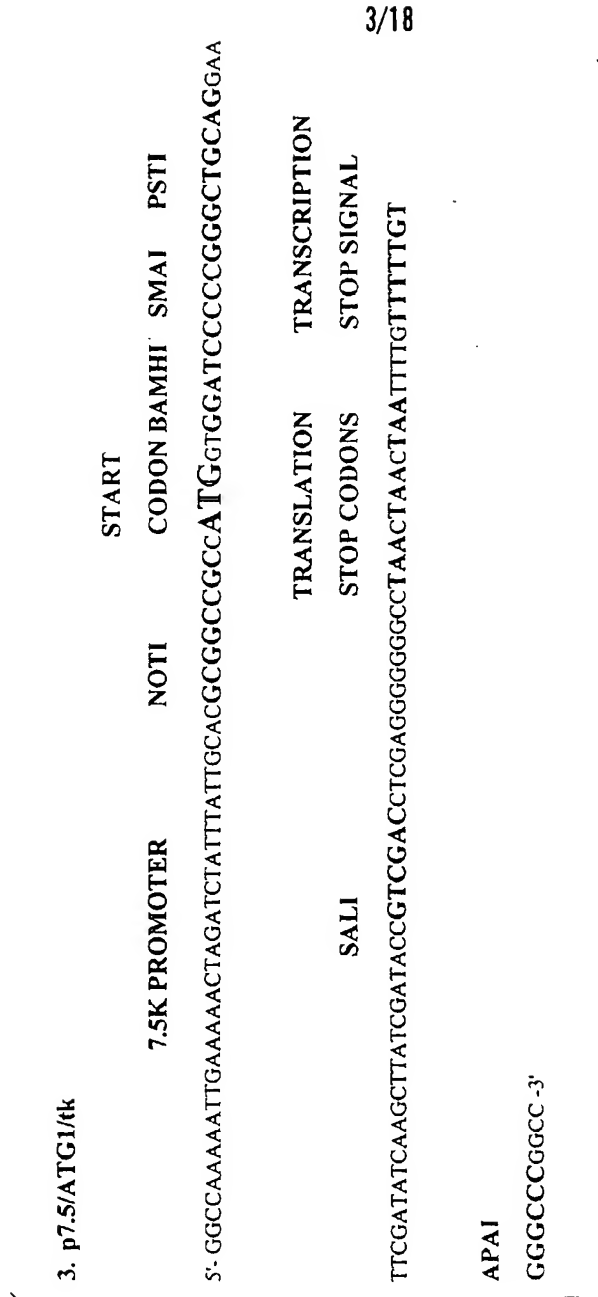


FIG. 2 (cont.)

4. p7.5/ATG2/tk

		START			
7.5K PROMOTER	NOTI	CODON	BAMHI	SMAI	PSTI
5'-GGCCAAAAATTGAAAAAAGTATCTATTTATTGCACGGGGCCGCGCATGAGTGGATCCCCCGGGCTGCAGGAA					
		TRANSLATION		TRANSCRIPTION	
SALI		STOP CODONS		STOP SIGNAL	
TTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCTAACTAAATTTGTTTTGT					
APAI					
GGGCCCCGGCC-3'					

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FIG. 2 (cont.)

5. p7.5/ATG3/tk	START				
	7.5K PROMOTER	NOTI	CODON	BAMHI SMAI	PSTI
5'- GGCCAAAAATTGAAAAAACTAGATCTATTATTGCACGGGGCCGCCcATGACGTGGATCCCCCGGGGCTGCAGGAA					
			TRANSLATION	TRANSCRIPTION	
	SALI		STOP CODONS	STOP SIGNAL	
TTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCCCTAACTAAATTGTTTTTGT					
APAI					
GGGCCCCGGCC -3'					

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FIG. 2 (cont.)

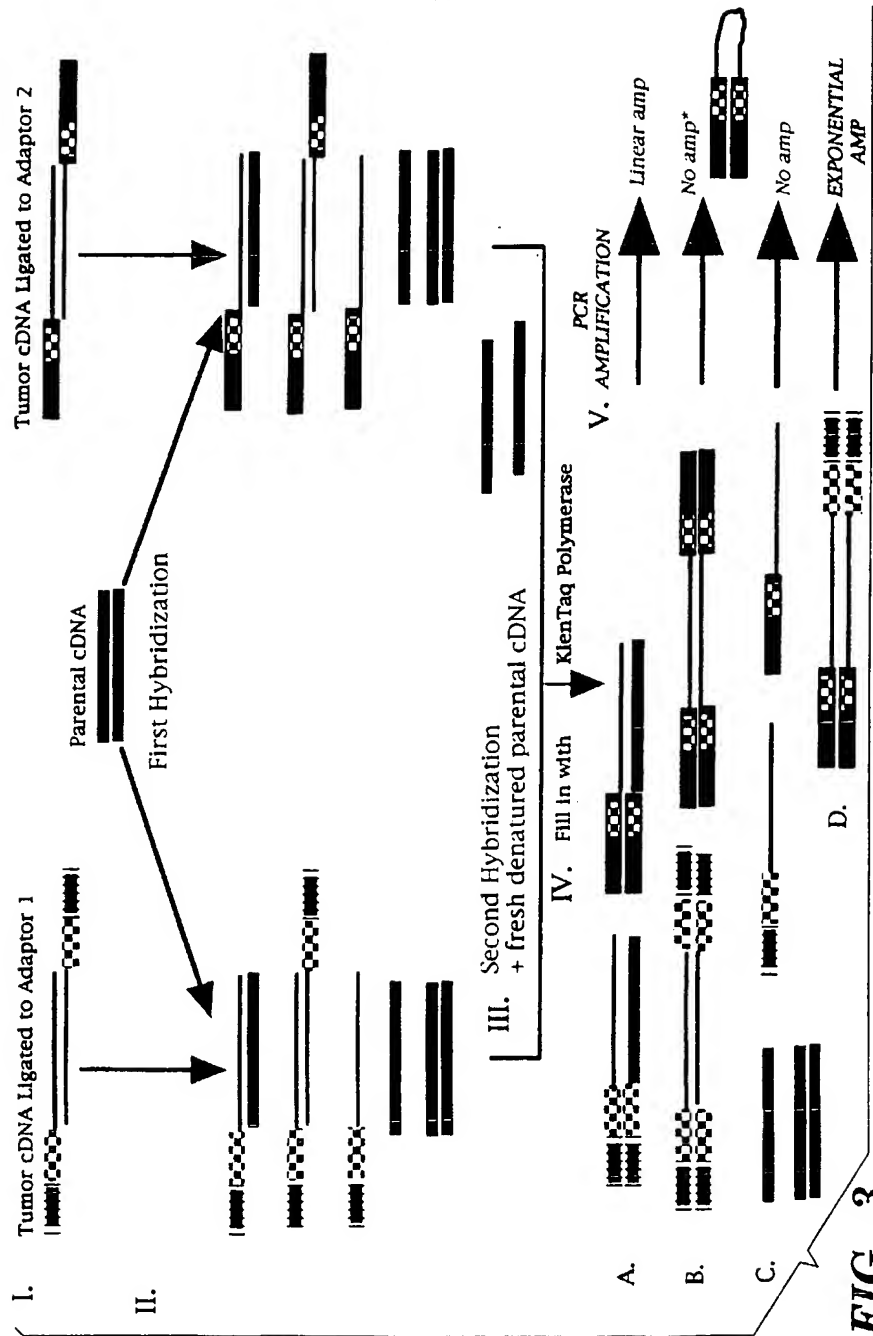


FIG. 3

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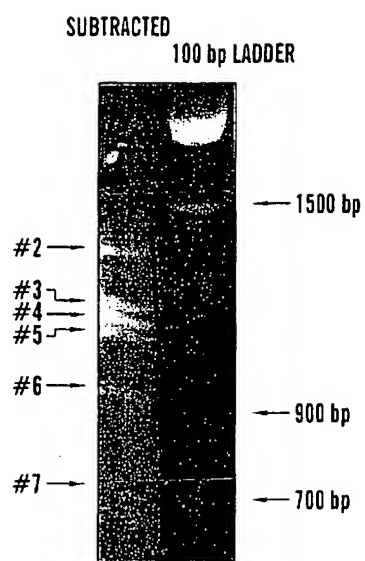
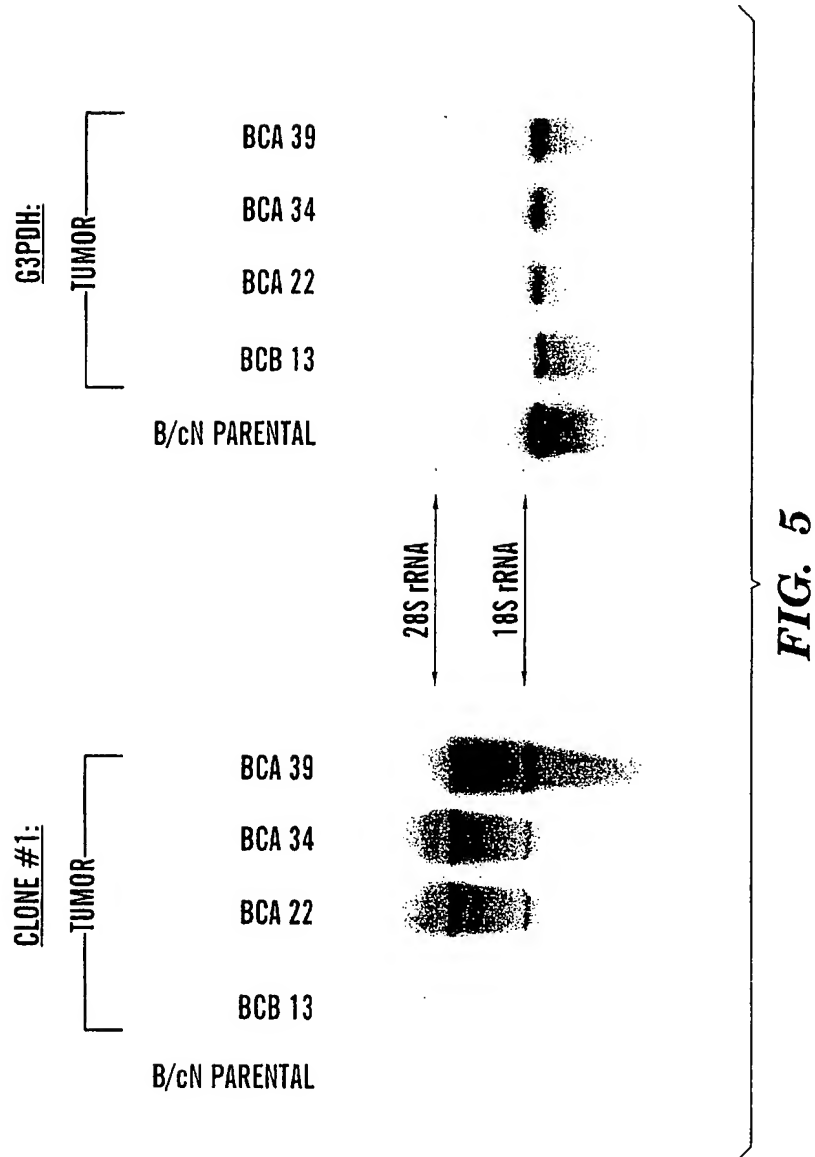
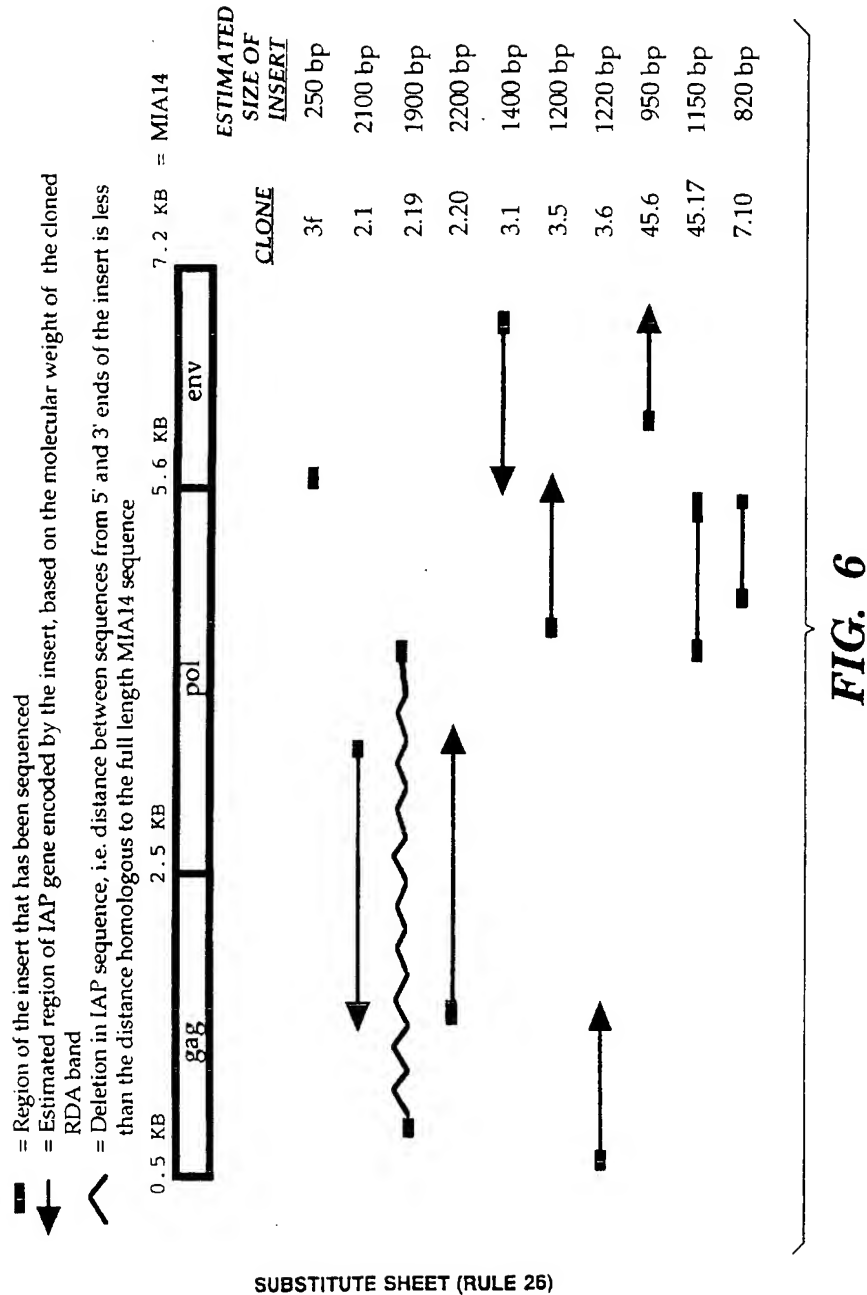


FIG. 4

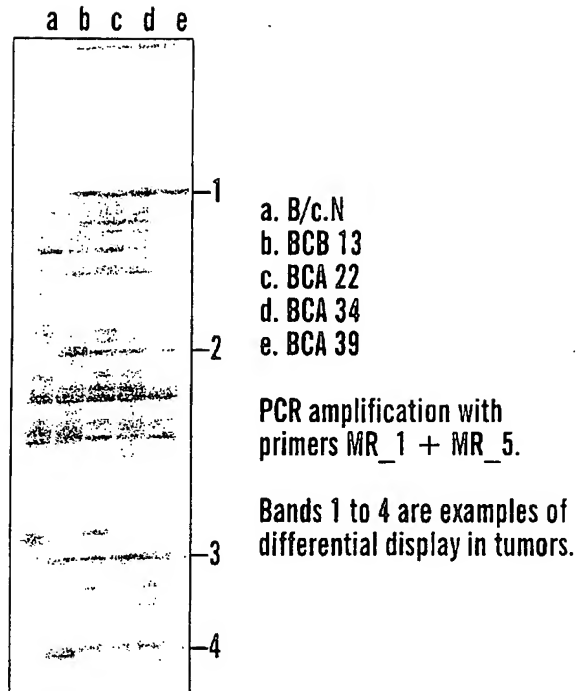
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*FIG. 7*

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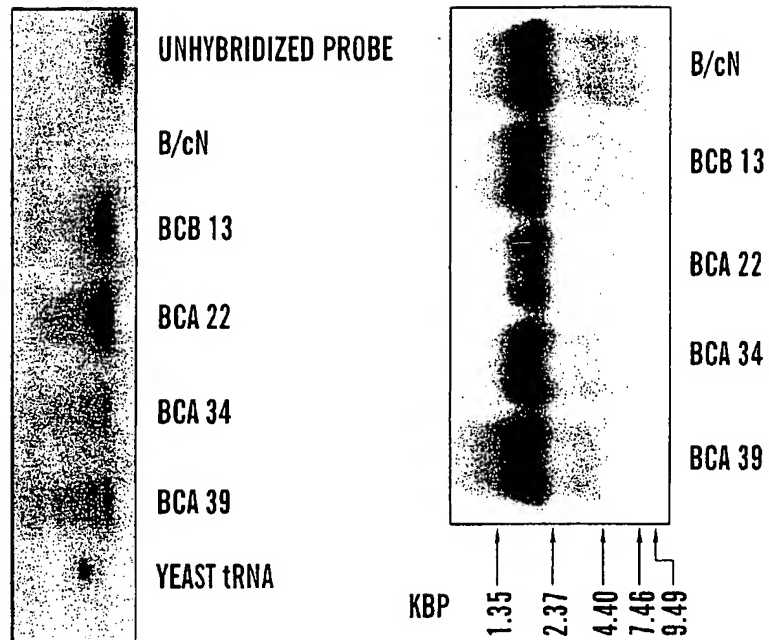
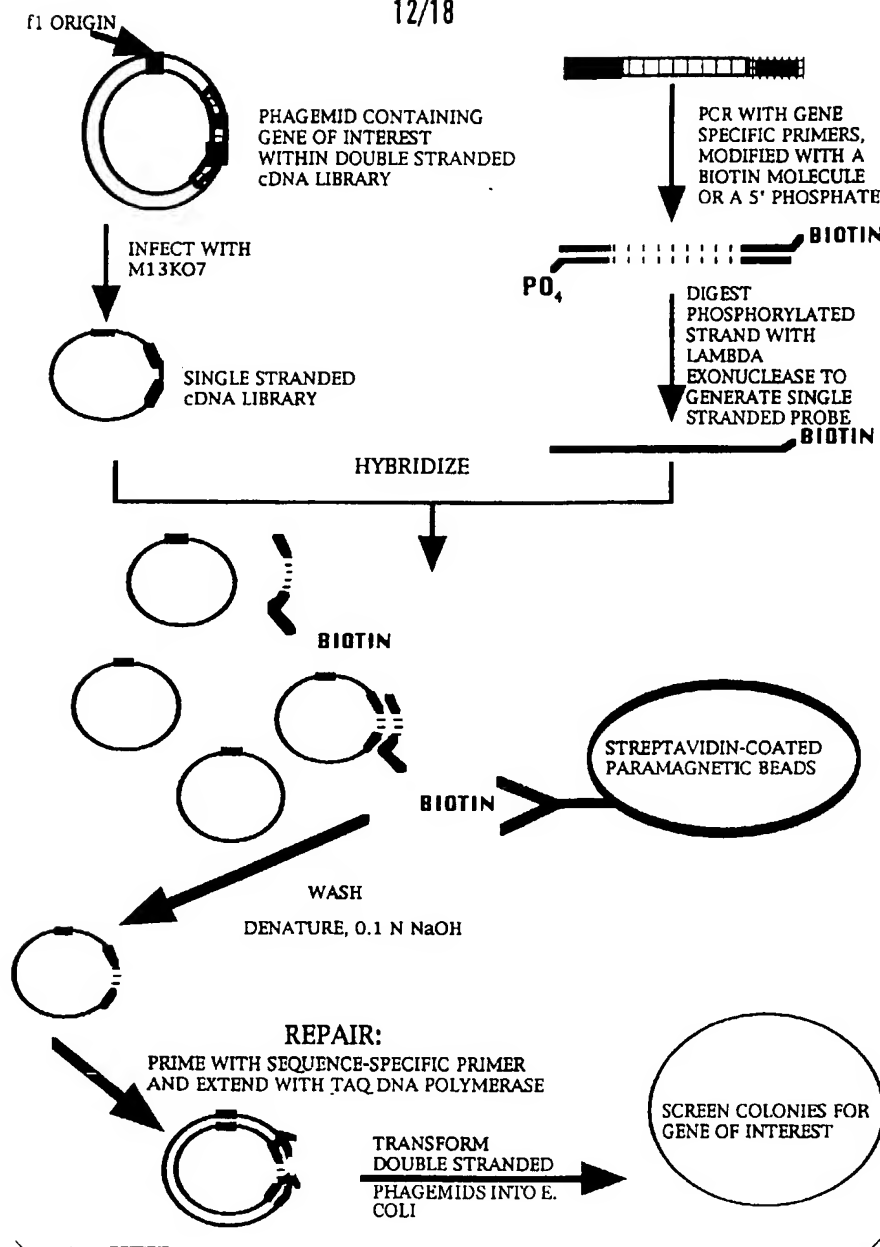


FIG. 8A

FIG. 8B

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**FIG. 9**

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Apal . Notl

λ WR WR vEL v7.5 vNotl/tk WR vEL v7.5 vNotl/tk

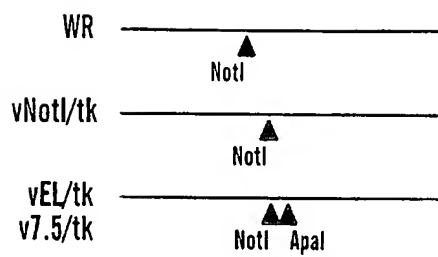
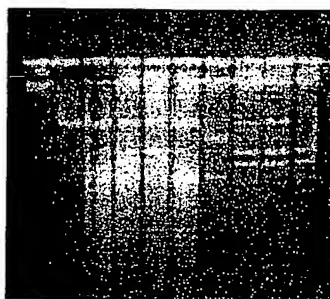


FIG. 10

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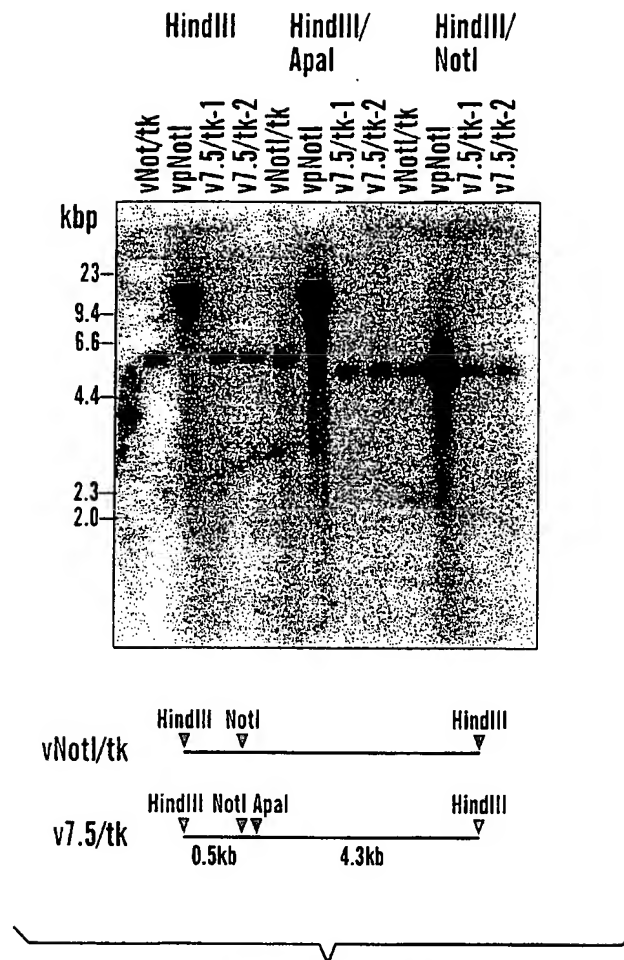


FIG. 11A

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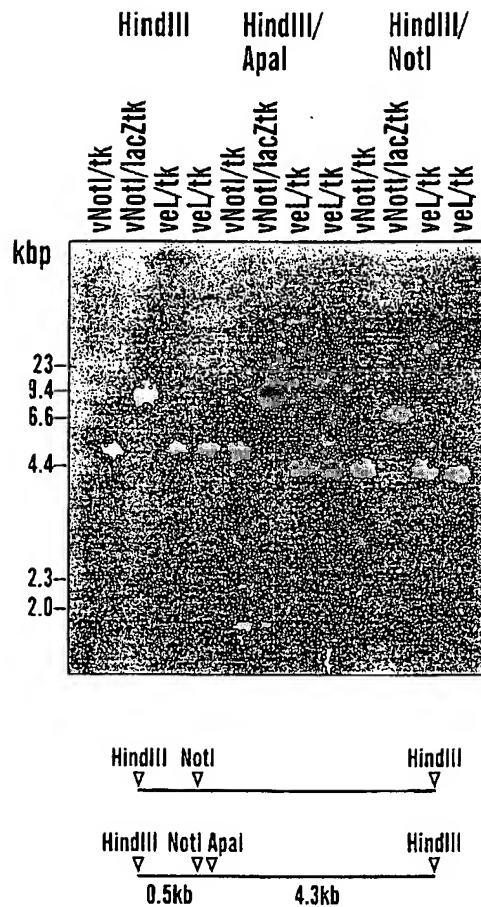


FIG. 11B

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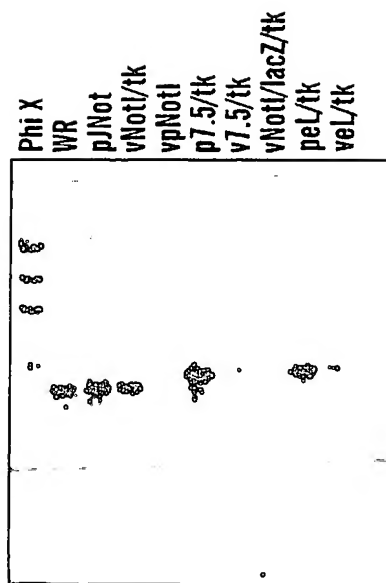
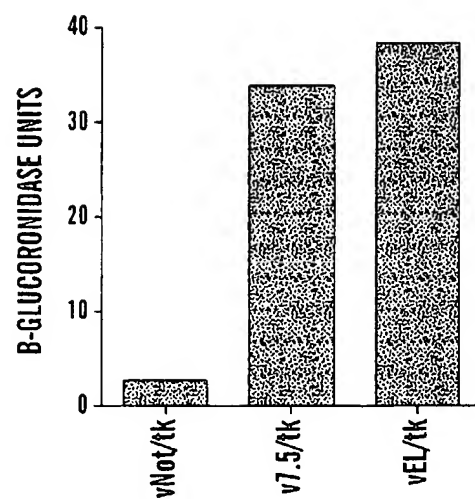
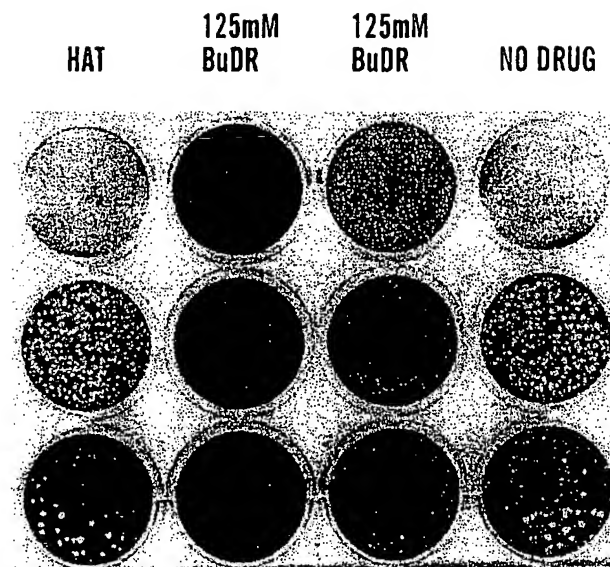


FIG. 12

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*FIG. 13*

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*FIG. 14*

INTERNATIONAL SEARCH REPORT

International Application No.
PCT/US 98/24029

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/10 C12N15/86 C12N5/06 C12Q1/68 A01K67/027

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C12Q A01K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 97 34143 A (UNIV BRITISH COLUMBIA :JEFFERIES WILFRED A (CA); GABATHULER REINHA) 18 September 1997	1-4,6,7, 11,14, 16-19, 22,25
Y	see claims 1-11 ---	5,15
X	R.-F. WANG ET AL.: "Development of a retrovirus-based complementary DNA expression system for the cloning of tumor antigens" CANCER RESEARCH, vol. 58, 15 August 1998, pages 3519-3525, XP002107625 AACR, BALTIMORE, US see the whole document --- -/--	1,4,7,8, 14,17, 22,25

☒ Further documents are listed in the continuation of box C☒ Patent family members are listed in annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"T" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"S" document member of the same patent family

Date of the actual completion of the international search

29 June 1999

Date of mailing of the international search report

12/07/1999

Name and mailing address of the ISA

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Authorized officer

Hornig, H

Form PCT/ISA/210 (second sheet) (July 1992)

page 1 of 2

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/24029

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	M. MERCHLINSKY ET AL.: "Construction and characterization of vaccinia direct ligation vectors" VIROLOGY, vol. 238, no. 2, 24 November 1997, pages 444-451, XP002107626 ACADEMIC PRESS, INC., NEW YORK, US	28-38
Y	see the whole document ---	5, 15
A	WO 97 26328 A (RPMS TECHNOLOGY LTD ;STAUSS HANS JOSEF (GB)) 24 July 1997 see the whole document ---	1-42
A	WO 95 33835 A (CHIRON CORP ;SELBY MARK (US); WALKER CHRISTOPHER (US)) 14 December 1995 see the whole document ---	1-42
A	WO 97 24438 A (ACTIVATED CELL THERAPY INC ;LAUS REINER (US); RUEGG CURTIS LANDON) 10 July 1997 see the whole document ---	1-42
A	TAKAHASHI H ET AL: "INDUCTION OF CD8+ CYTOTOXIC T CELLS BY IMMUNIZATION WITH PURIFIED HIV-1 ENVELOPE PROTEIN IN ISCOMS" NATURE, vol. 344, 26 April 1990, pages 873-875, XP002031410 see the whole document ---	1-42
A	"Clonetech PCR-Select™ Subtraction" CLONETECH CATALOG 98/99, 1998, page 24 XP002107627 Clonetech laboratories, Palo Alto, Ca, US cited in the application see figure 2.4 ---	1-42
A	US 5 804 382 A (YANG MEIHENG ET AL) 8 September 1998 see the whole document ---	1-42
A	D.M. SAHASRABUDHE ET AL.: "Shared T cell-defined antigens on independently derived tumors" J. OF IMMUNOLOGY, vol. 151, no. 11, 1 December 1993, pages 6302-6310, XP002107628 WAVERLY PRESS, BALTIMORE, MD, US cited in the application see the whole document -----	1-42

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/ 24029

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☒ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/SA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-27,39-42

A method for identifying a target epitope comprising screening products from an expression library generated from DNA or RNA derived from cells expressing the target epitope with cytotoxic T cells generated against the cell to identify DNA clones expressing the target epitope; a transgenic animal tolerized with a non-tumorigenic cell line that does not express costimulatory activity; a cytotoxic T cell derived from said transgenic animal;

2. Claims: 28-38

A viral vector containing a DNA insert flanked by unique sites for restriction enzymes positioned so that religation of the viral vector arms is prevented and the orientation of the insert DNA is fixed and the DNA insert is operatively associated with a strong regulatory element.

INTERNATIONAL SEARCH REPORT

information on patent family members

International Application No

PCT/US 98/24029

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9734143 A	18-09-1997	US 5792604 A AU 2088997 A EP 0888540 A US 5845028 A	11-08-1998 01-10-1997 07-01-1999 01-12-1998
WO 9726328 A	24-07-1997	AU 1394497 A CA 2243235 A EP 0879282 A	11-08-1997 24-07-1997 25-11-1998
WO 9533835 A	14-12-1995	AU 2656295 A CA 2191362 A EP 0802980 A JP 10501136 T	04-01-1996 14-12-1995 29-10-1997 03-02-1998
WO 9724438 A	10-07-1997	AU 1338097 A CA 2241373 A EP 0870022 A	28-07-1997 10-07-1997 14-10-1998
US 5804382 A	08-09-1998	NONE	